



# **STIC Search Report**

## **Biotech-Chem Library**

**STIC Database Tracking Number: 192503**

**TO: Ruixiang Li**  
**Location: rem/4D75/4C70**  
**Art Unit: 1646**  
**Thursday, June 15, 2006**  
**Case Serial Number: 10/694438**

**From: Vira David**  
**Location: Biotech-Chem Library**  
**REM-1A41**  
**Phone: (571)272-1972**

**Virajita.David@uspto.gov**

### **Search Notes**

Examiner Li,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Vira David  
Intern  
STIC Biotech/Chem Library  
(571)272-1110

78733

STIC-Biotech/ChemLib

192503

mg

From: Li, Ruixiang  
Sent: Saturday, June 10, 2006 8:43 AM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search of Application No.10/694,438

Please do:

An oligomer search of SEQ ID NO: 2 against both commercial and interference amino acid databases.

Thank you very much!

Ruixiang Li  
GAU 1646  
REM 4D75  
Mail Box 4C70  
(571) 272-0875

\*\*\*\*\*

Searcher: \_\_\_\_\_  
Searcher Phone: \_\_\_\_\_  
Date Searcher Picked up: \_\_\_\_\_  
Date completed: \_\_\_\_\_  
Searcher Prep Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search  
NA# \_\_\_\_\_ AA# \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure #: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (Specify): \_\_\_\_\_

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 12, 2006, 12:17:23 ; Search time 17 Seconds  
(without alignments)  
528.040 Million cell updates/sec

Title: US-10-694-438-2  
Perfect score: 710  
Sequence: 1 MERTAGKELALPLQDWGE.....RDFMLRKSGRTNLSVSPS 710

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 64916 seqs, 12643201 residues

Word size : 1

Total number of hits satisfying chosen parameters: 64909

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA New:

- 1: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_NEW\_PUB\_PEP.\*
- 2: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US06\_NEW\_PUB\_PEP.\*
- 3: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US07\_NEW\_PUB\_PEP.\*
- 4: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_NEW\_PUB\_PEP.\*
- 5: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/PCT\_NEW\_PUB\_PEP.\*
- 6: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10\_NEW\_PUB\_PEP.\*
- 7: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_NEW\_PUB\_PEP.\*
- 8: /EMC\_Celerra\_SIDS3/ptodata/2/pubpaa/US60\_NEW\_PUB\_PEP.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
|------------|-------|-------------|--------|-------|---------------------|
| 1          | 207   | 29.2        | 208    | 7     | US-11-293-697-3953  |
| 2          | 8     | 1.1         | 133    | 6     | US-10-953-349-20651 |
| 3          | 8     | 1.1         | 231    | 6     | US-10-953-349-20650 |
| 4          | 8     | 1.1         | 265    | 6     | US-10-953-349-20649 |
| 5          | 8     | 1.1         | 358    | 7     | US-11-293-697-3662  |
| 6          | 8     | 1.1         | 575    | 6     | US-10-953-349-6447  |
| 7          | 8     | 1.1         | 627    | 6     | US-10-953-349-6446  |
| 8          | 8     | 1.1         | 642    | 6     | US-10-505-928-259   |
| 9          | 8     | 1.1         | 664    | 6     | US-10-953-349-6445  |
| 10         | 7     | 1.0         | 77     | 6     | US-10-953-349-36948 |
| 11         | 7     | 1.0         | 78     | 6     | US-10-953-349-36948 |
| 12         | 7     | 1.0         | 89     | 6     | US-10-953-349-36483 |
| 13         | 7     | 1.0         | 91     | 6     | US-10-953-349-29384 |
| 14         | 7     | 1.0         | 103    | 7     | US-11-293-697-4841  |
| 15         | 7     | 1.0         | 111    | 6     | US-10-953-393-3     |
| 16         | 7     | 1.0         | 119    | 6     | US-10-953-349-30754 |
| 17         | 7     | 1.0         | 134    | 6     | US-10-953-349-22783 |
| 18         | 7     | 1.0         | 138    | 6     | US-10-953-349-39282 |
| 19         | 7     | 1.0         | 154    | 6     | US-10-953-349-22782 |
| 20         | 7     | 1.0         | 154    | 6     | US-10-953-349-25483 |
| 21         | 7     | 1.0         | 159    | 7     | US-11-293-697-2997  |
| 22         | 7     | 1.0         | 164    | 6     | US-10-953-349-22781 |
| 23         | 7     | 1.0         | 175    | 6     | US-10-953-349-17915 |
| 24         | 7     | 1.0         | 183    | 6     | US-10-953-349-5438  |
| 25         | 7     | 1.0         | 186    | 6     | US-10-953-349-39281 |

## ALIGNMENTS

### RESULT 1

US-11-293-697-3953  
; Sequence 1953, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cdna  
; FILE REFERENCE: HI-A0106  
; CURRENT APPLICATION NUMBER: US/11/293.697  
; PRIOR FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108.260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3953  
; LENGTH: 208  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-3953

Query Match 29.2%; Score 207; DB 7; Length 208;  
Best Local Similarity 100.0%; Pred. No. 7e-186;  
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 237 | MPQGPQLLDFSVDEVAEQTLIDLELFSKVLVECLGSVMSQDRPGGAAGASPTVRATVA  | 296 |
| Db | 1   | MPQGPQLLDFSVDEVAEQTLIDLELFSKVLVECLGSVMSQDRPGGAAGASPTVRATVA  | 60  |
| Qy | 297 | QFNTVTGCVLGSVLGAPGLAAPQRAQRLNFKWIRIAQRCRELNFSSRLAISALQSNPIY | 356 |
| Db | 61  | QFNTVTGCVLGSVLGAPGLAAPQRAQRLNFKWIRIAQRCRELNFSSRLAISALQSNPIY | 120 |
| Qy | 357 | RLKRSWGAVSREPLSTFRKLSQIFSDNNHLSREILFQEAEGSQEEDNTPGSLSPKP    | 416 |
| Db | 121 | RLKRSWGAVSREPLSTFRKLSQIFSDNNHLSREILFQEAEGSQEEDNTPGSLSPKP    | 180 |
| Qy | 417 | PPGFPVPLGFTFLDVLMDLTALPDMLE                                 | 443 |
| Db | 181 | PPGFPVPLGFTFLDVLMDLTALPDMLE                                 | 207 |

### RESULT 2

US-10-953-349-20651  
; Sequence 20651, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; TITLE OF INVENTION: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20651  
; LENGTH: 133  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-20651

Query Match 1.1%; Score 8; DB 6; Length 133;  
Best Local Similarity 100.0%; Pred. No. 3.9;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 SQIFSDEN 384  
Db 119 SQIFSDEN 126

## RESULT 3

US-10-953-349-20650  
; Sequence 20650, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20650  
; LENGTH: 231  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-20650

Query Match 1.1%; Score 8; DB 6; Length 231;  
Best Local Similarity 100.0%; Pred. No. 6.5;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 SQIFSDEN 384  
Db 217 SQIFSDEN 224

## RESULT 4

US-10-953-349-20649  
; Sequence 20649, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 20649  
; LENGTH: 265  
; TYPE: PRT  
; ORGANISM: Glycine max  
US-10-953-349-20649

Query Match 1.1%; Score 8; DB 6; Length 265;  
Best Local Similarity 100.0%; Pred. No. 7.3;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 377 SQIFSDEN 384

Db 251 SQIFSDEN 258

## RESULT 5

US-11-293-697-3662  
; Sequence 3662, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3662  
; LENGTH: 358  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-3662

Query Match 1.1%; Score 8; DB 7; Length 358;  
Best Local Similarity 100.0%; Pred. No. 9.6;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 550 SVSPGSP 557  
Db 288 SVSPGSP 295

## RESULT 6

US-10-953-349-6447  
; Sequence 6447, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6447  
; LENGTH: 575  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-6447

Query Match 1.1%; Score 8; DB 6; Length 575;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 544 PSSPTSSV 551  
Db 485 PSSPTSSV 492

## RESULT 7

US-10-953-349-6446  
; Sequence 6446, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: ENCODED THERBY  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 6446  
; LENGTH: 627  
; TYPE: PRT  
; ORGANISM: Arabidopsis thaliana  
US-10-953-349-6446

Query Match 1.1%; Score 8; DB 6; Length 627;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 544 PSSPTSSV 551  
|||||  
Db 537 PSSPTSSV 544

## RESULT 8

US-10-505-928-259  
; Sequence 259, Application US/10505928  
; Publication No. US20060088532A1

; GENERAL INFORMATION:  
; APPLICANT: Ludwig Institute for Cancer Research et al.  
; TITLE OF INVENTION: LYMPHATIC ENDOTHELIAL GENES

; FILE REFERENCE: 28967/39178

; CURRENT APPLICATION NUMBER: US/10/505,928

; CURRENT FILING DATE: 2004-08-27

; PRIOR APPLICATION NUMBER: US 60/363,019

; NUMBER OF SEQ ID NOS: 866

; SOFTWARE: PatentIn 3.2

; SEQ ID NO 259

; LENGTH: 642

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-505-928-259

## Query Match

Best Local Similarity 1.1%; Score 8; DB 6; Length 642;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 WGEETEDG 24  
|||||  
Db 211 WGEETEDG 218

## RESULT 9

US-10-953-349-6445

; Sequence 6445, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 6445

; LENGTH: 664

; TYPE: PRT

; ORGANISM: Arabidopsis thaliana

US-10-953-349-6445

## Query Match

Best Local Similarity 1.1%; Score 8; DB 6; Length 664;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 544 PSSPTSSV 551  
|||||  
Db 574 PSSPTSSV 581

## RESULT 10

US-10-953-349-36948

; Sequence 36948, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 36948

; LENGTH: 77

; TYPE: PRT

; ORGANISM: Zea mays subsp. mays

US-10-953-349-36948

## Query Match

Best Local Similarity 1.0%; Score 7; DB 6; Length 77;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 552 SPGSPPS 558  
|||||  
Db 56 SPGSPPS 62

## RESULT 11

US-10-953-349-36484

; Sequence 36484, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 36484

; LENGTH: 78

; TYPE: PRT

; ORGANISM: Zea mays subsp. mays

US-10-953-349-36484

## Query Match

Best Local Similarity 1.0%; Score 7; DB 6; Length 78;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 534 SSSPPSGS 540  
|||||  
Db 15 SSSPPSGS 21

## RESULT 12

US-10-953-349-36483

; Sequence 36483, Application US/10953349

; Publication No. US20060107345A1

; GENERAL INFORMATION:

; APPLICANT: ALEXANDROV, Nikolai et al.

; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES

; FILE REFERENCE: 2750-1579PUS2

; CURRENT APPLICATION NUMBER: US/10/953,349

; CURRENT FILING DATE: 2004-09-30

; NUMBER OF SEQ ID NOS: 40252

; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 36483

; LENGTH: 89

; TYPE: PRT

; ORGANISM: Zea mays subsp. mays

US-10-953-349-36483

US-10-953-349-36483

Query Match 1.0%; Score 7; DB 6; Length 89;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 534 SSSPSGS 540  
DB 26 SSSPSGS 32

## RESULT 13

US-10-953-349-29384  
; Sequence 29384, Application US/10953349  
; Publication No. US20060107345A1  
; GENERAL INFORMATION:  
; APPLICANT: ALEXANDROV, Nikolai et al.  
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES  
; FILE REFERENCE: 2750-1579PUS2  
; CURRENT APPLICATION NUMBER: US/10/953,349  
; CURRENT FILING DATE: 2004-09-30  
; NUMBER OF SEQ ID NOS: 40252  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 29384  
; LENGTH: 91  
; TYPE: PRT  
; ORGANISM: Triticum aestivum  
US-10-953-349-29384

Query Match 1.0%; Score 7; DB 6; Length 91;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 544 PSSPTSS 550  
DB 46 PSSPTSS 52

## RESULT 14

US-11-293-697-4841  
; Sequence 4841, Application US/11293697  
; Publication No. US20060105376A1  
; GENERAL INFORMATION:  
; APPLICANT: HELIX RESEARCH INSTITUTE  
; TITLE OF INVENTION: Novel full length cDNA  
; FILE REFERENCE: H1-A0106  
; CURRENT APPLICATION NUMBER: US/11/293,697  
; CURRENT FILING DATE: 2005-12-05  
; PRIOR APPLICATION NUMBER: US/10/108,260  
; PRIOR FILING DATE: 2002-03-28  
; NUMBER OF SEQ ID NOS: 5458  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4841  
; LENGTH: 103  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-293-697-4841

Query Match 1.0%; Score 7; DB 7; Length 103;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 DRPGAAG 286  
DB 46 DRPGAAG 52

## RESULT 15

US-10-953-393-3  
; Sequence 3, Application US/10953393  
; Publication No. US2006008851A1  
; GENERAL INFORMATION:

; APPLICANT: Ayyavoo, Velpandi  
; APPLICANT: Patel, Mamata  
; APPLICANT: Kieber-Emmons, Thomas  
; APPLICANT: Weiner, David B.  
; APPLICANT: Mahalingam, Sundaramy  
; TITLE OF INVENTION: Functional Fragments of HIV-1 VPR Protein and Methods  
; FILE REFERENCE: UPN-4023  
; CURRENT APPLICATION NUMBER: US/10/953,393  
; CURRENT FILING DATE: 2004-09-29  
; PRIOR APPLICATION NUMBER: US/09/485,421  
; PRIOR FILING DATE: 2000-10-05  
; PRIOR APPLICATION NUMBER: 60/055,754  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 111  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Novel Sequence  
US-10-953-393-3

Query Match 1.0%; Score 7; DB 6; Length 111;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 118 PPPPPPG 124  
DB 104 PPPPPPG 110

Search completed: June 12, 2006, 12:20:40  
Job time : 17 secs

November 2005

Published\_Applications\_Nucleic\_Acid\_and\_Published\_Applications\_Amino\_Acid database searches now generate two sets of results each. The Published\_Applications databases have been split into two parts to reduce the amount of time required for their daily updates. This results in more machine time being available for processing searches.

Newly published applications will appear in the Published\_Applications\_New databases; older published applications make up the Published\_Applications\_Main databases.

Searches run against Nucleic\_Acid\_Published\_Applications produce two sets of results, with the extensions **.rnpbm** (Published\_Applications\_NA\_Main) and **.rnpbn** (Published\_Applications\_NA\_New). Searches run against Amino\_Acid\_Published\_Applications produce two sets of results, with the extensions **.rapbm** (Published\_Applications\_AA\_Main) and **.rapbn** (Published\_Applications\_AA\_New).

## Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC search.

**When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.**



GenCore version 5.1.9  
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OM protein - protein search, using sw model

Run on: June 12, 2006, 11:56:13 / Search time 304 Seconds  
(without alignments)

2160.398 Million cell updates/sec

Title: US-10-694-438-2

Perfect score: 710

Sequence: 1 MERTAGKELALAPLQDWGEE.....RDFMLRRKRGTRNTLSVSPS 710

Scoring table: OLIGO

Searched: 2849598 seqs, 925015592 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: UniProt-7.2.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description  |
|------------|-------|-------------|--------|-------|--------------|
| 1          | 609   | 85.8        | 710    | 2     | Q3MIN7_HUMAN |
| 2          | 402   | 56.6        | 497    | 2     | Q8TEP0_HUMAN |
| 3          | 447   | 6.6         | 343    | 2     | Q9DBL8_MOUSE |
| 4          | 47    | 6.6         | 505    | 2     | Q6KAR7_MOUSE |
| 5          | 47    | 6.6         | 687    | 2     | Q8BKJ3_MOUSE |
| 6          | 47    | 6.6         | 709    | 2     | Q3UY15_MOUSE |
| 7          | 47    | 6.6         | 709    | 2     | Q924M8_MOUSE |
| 8          | 47    | 6.6         | 709    | 2     | Q9JID4_MOUSE |
| 9          | 17    | 2.4         | 309    | 2     | Q5T7U6_HUMAN |
| 10         | 17    | 2.4         | 411    | 2     | Q8N4Y1_HUMAN |
| 11         | 17    | 2.4         | 555    | 2     | Q3UEA9_MOUSE |
| 12         | 17    | 2.4         | 625    | 2     | Q8NF31_HUMAN |
| 13         | 17    | 2.4         | 745    | 2     | Q9P2N8_HUMAN |
| 14         | 17    | 2.4         | 824    | 2     | Q8TEK9_HUMAN |
| 15         | 17    | 2.4         | 840    | 2     | Q3UY99_MOUSE |
| 16         | 17    | 2.4         | 852    | 2     | Q3UY99_MOUSE |
| 17         | 17    | 2.4         | 852    | 2     | Q8R077_MOUSE |
| 18         | 17    | 2.4         | 859    | 2     | Q6KHL1_HUMAN |
| 19         | 17    | 2.4         | 895    | 1     | Q3XZ3_MOUSE  |
| 20         | 17    | 2.4         | 895    | 1     | Q3XZ3_MOUSE  |
| 21         | 17    | 2.4         | 902    | 2     | Q6PCB1_HUMAN |
| 22         | 17    | 2.4         | 907    | 2     | Q3TWC1_MOUSE |
| 23         | 17    | 2.4         | 913    | 2     | Q6ZSD5_HUMAN |
| 24         | 17    | 2.4         | 914    | 1     | Q6ZSD5_HUMAN |
| 25         | 17    | 2.4         | 914    | 1     | Q6ZSD5_HUMAN |
| 26         | 17    | 2.4         | 924    | 2     | Q5T7V4_HUMAN |
| 27         | 15    | 2.1         | 924    | 2     | Q6ZPU1_MOUSE |
| 28         | 13    | 1.8         | 782    | 2     | Q4S7S0_TETNG |
| 29         | 12    | 1.7         | 804    | 2     | Q4RPV7_TETNG |
| 30         | 11    | 1.5         | 78     | 2     | Q6P112_BRARE |
| 31         | 11    | 1.5         | 359    | 2     | Q57412_TETFL |
|            |       |             |        |       | Q9DE48_BRARE |

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|----|----|-----|-----|---|--------------|--------------------|
| 32 | 11 | 1.5 | 742 | 2 | Q4SD50_TETNG | Q4SD50_tetradon n  |
| 33 | 11 | 1.5 | 766 | 2 | Q5RDR4_PONPY | Q5RDR4_pongo pygma |
| 34 | 11 | 1.5 | 768 | 1 | Q6L1_HUMAN   | Q6L1_homo sapien   |
| 35 | 11 | 1.5 | 768 | 1 | Q6L1_MOUSE   | Q6L1_mus muscicu   |
| 36 | 11 | 1.5 | 768 | 2 | Q5VU93_HUMAN | Q5VU93_homo sapien |
| 37 | 11 | 1.5 | 768 | 2 | Q8VD09_MOUSE | Q8VD09_m rat guani |
| 38 | 11 | 1.5 | 768 | 2 | Q5Z1Y0_CHICK | Q5Z1Y0_gallus gall |
| 39 | 11 | 1.5 | 803 | 2 | Q5VU94_HUMAN | Q5VU94_homo sapien |
| 40 | 11 | 1.5 | 803 | 2 | Q7Z3U6_HUMAN | Q7Z3U6_homo sapien |
| 41 | 10 | 1.4 | 372 | 2 | Q5C1L6_SCHJA | Q5C1L6_schistosoma |
| 42 | 10 | 1.4 | 765 | 2 | Q5TPE0_ANOGA | Q5TPE0_anopheles g |
| 43 | 10 | 1.4 | 774 | 2 | Q86B12_DROME | Q86B12_drosophila  |
| 44 | 10 | 1.4 | 774 | 2 | Q9GR11_DROME | Q9GR11_drosophila  |
| 45 | 10 | 1.4 | 860 | 2 | Q19852_CAEEL | Q19852_caenorhabdi |

#### ALIGNMENTS

RESULT 1  
Q3MIN7\_HUMAN PRELIMINARY; PRT; 710 AA.  
AC Q3MIN7;  
DT 25-OCT-2005, integrated into UniProtKB/TrEMBL.  
DT 25-OCT-2005, sequence version 1.  
DT 21-FEB-2006, entry version 5.  
DE Ral guanine nucleotide dissociation stimulator-like 3.  
GN Name=RG1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung and heart;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
RA Datchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Uding T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millaby S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huij S.W.,  
RA Vallatton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.W.,  
RA Buttefield Y.S.N., Krzywicki M.I., Skalska U., Smilins D.E.,  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung and heart;  
RG NIH MGC Project;  
RL Submitted (Aug-2005) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Lung and heart;  
RG NIH MGC Project;  
RL Submitted (Jan-2006) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NonDerivs License  
CC EMBL/BC101756; AA101757.1; -; mRNA.  
DR EMBL/BC11958; AA11959.1; -; mRNA.

| DT | 01-JUN-2002, integrated into UniProtKB/TrEMBL.   |
|----|--|
| DT | 01-JUN-2002, sequence version 1.   |
| DT | 07-FEB-2006, entry version 15.   |
| DE | FLJ00153 protein (Fragment).   |
| GN | Name=FLJ00153.   |
| OS | homo sapiens (Human).  |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  |
| OC | Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;   |
| OC | Homo.  |
| OX | NCBI_TaxId=9606;   |
| RN | (1)  |
| RP | NUCLEOTIDE SEQUENCE.   |
| RC | TISSUE=Spleen;   |
| RA | Jikuya H., Takano T., Nomura N., Kikuno R., Nagase T., Ohara O.;   |
| RL | Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  |
| CC | -----  |
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| CC | -----  |
| DR | EMBL; AK074082; BAB84908.1; -, mRNA.   |
| DR | HSSP; Q03386; ILFD.  |
| DR | Ensembl; ENSG00000187266; Homo sapiens.  |
| DR | GO; GO:0005085; P:guanylnucleotide exchange factor activity, IEA.  |
| DR | GO; GO:0007264; P:small GTPase mediated signal transduction, IEA.  |
| DR | InterPro; IPR001591, RA.   |
| DR | InterPro; IPR001895, RasGRF_CDC25.   |
| DR | Pfam; PF00718; RA; 1.  |
| DR | Pfam; PF00617; RasGEF; 1.  |
| DR | SMART; SM00147; RasGEF; 1.   |
| DR | PROSITE; PS00720; RasGEF; 1.   |
| DR | PROSITE; PS50009; RasGEF_CAT; 1.   |
| FT | NON TER 1 1  |
| SQ | SEQUENCE 497 AA; 54312 MW; F78318B92826F537 CRC64;   |

DT 01-JUN-2001, sequence version 1.  
 DT 07-FEB-2006, entry version 20.  
 DE Adult male liver cDNA, RIKEN full-length enriched library,  
 DE clone:1300003D20 product:similar to RALGDS-RELATED EFFECTOR PROTEIN OF  
 DE M-RAS.  
 GN Name=Rgl3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_taxid=10090;  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=liver;  
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";  
 RL Methods Enzymol. 303:19-44(1999).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=liver;  
 RC PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
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 RA Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 RA Bansal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
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 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Paulkner G.,  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
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 RA Fukuoka S., Kanamori-Katayama M., Suzuki M., Aoki J., Arikawa T.,  
 RA Iida J., Imanura K., Itoh M., Kato T., Kawai H., Kawagashira N.,  
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimura N.,  
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Wataniki A., Okamura-Oho Y., Suzuki H., Kawai J.,  
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 RL Science 309:1559-1563(2005).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=liver;  
 RC PubMed=16141073; DOI=10.1126/science.1112009;  
 RA RIKEN Genome Exploration Research Group, and Genome Science Group  
 RG "Genome Network Core Team) and the FANTOM Consortium;  
 RT "Antisense transcription in the Mammalian Transcriptome.";  
 RL Science 309:1564-1566(2005).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=liver;  
 RC MEDLINE=23354683; PubMed=12466851; DOI=10.1038/nature01266;  
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 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,  
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 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
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 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";  
 RL Nature 420:563-573(2002).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=liver;  
 RC MEDLINE=21085560; PubMed=11217651; DOI=10.1038/35055500;  
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 RA Arikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
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 RA Schirni L.M., Stablil F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Bash G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli U., Moudarts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schonbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmong L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
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 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=liver;  
 RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
 RA Carninci P., Shibata Y., Hayatsu N., Suganaka Y., Shibata K., Itoh M.,  
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 RL Genome Res. 10:1617-1630(2000).  
 RN NUCLEOTIDE SEQUENCE.  
 RP STRAIN=C57BL/6J; TISSUE=liver;  
 RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
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 RA Kono H., Akiyama J., Nishi K., Kitsuaki T., Tashiro H., Itoh M.,  
 RA Sumi N., Iehi Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,  
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RIKEN Integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer."  
 RL Genome Res. 10:1757-1771(2000).  
 RN [8]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Liver;  
 RA Aachai J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
 Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
 Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hirakawa T., Hori F.,  
 Imotani K., Ishii Y., Itoh M., Itawa M., Kasukawa T., Kato H.,  
 Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
 Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
 Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
 Sano H., Sasaki D., Shibata K., Shibata Y., Shingawa A., Shiraki T.,  
 Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
 Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
 Muramatsu M., Hayashizaki Y.,  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
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 CC  
 DR EMBL: AK004876; BAB23634.1; -. mRNA.  
 DR MGI: MGI:1918996; Rg13.  
 DR GO: GO:0005515; F:Protein binding; IPI.  
 DR GO: GO:0008321; F:Rat guanyl-nucleotide exchange factor activity; IDA.  
 DR GO: GO:0017016; F:Ras GTPase binding; IDA.  
 DR GO: GO:0007218; P:neuropeptide signaling pathway; RCA.  
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; TAS.  
 DR InterPro: IPR001895; RasGRF\_CDC25.  
 DR Pfam: PF006417; RasGEF\_1.  
 DR SMART: SM00147; RasGEF\_1.  
 DR PROSITE: PS50009; RasGEF\_CAT, 1.  
 DR SEQUENCE 343 AA; 37517 MW; B66A576AE9B973A9 CRC64;  
 SQ  
 Query Match 6.6%; Score 47; DB 2; Length 343;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-35;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 325 EKWIRIAORCRELRNPSLRATLSALOSNPYRLKRSWGAVSREPLS 371  
 DB 227 EKWIRIAORCRELRNPSLRATLSALOSNPYRLKRSWGAVSREPLS 273  
 RESULT 4  
 ID Q6KAR7\_MOUSE PRELIMINARY; PRT; 505 AA.  
 AC Q6KAR7;  
 DT 05-JUL-2004, integrated into UniProtKB/TrEMBL.  
 DT 05-JUL-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 11.  
 DE MFL000153 protein (Fragment).  
 GN Name=Rg13; Synonyms=MFLJ00153;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RN NUCLEOTIDE SEQUENCE.  
 RP TISSUE=Embryonic tail;  
 RA Okazaki N., Kikuno R., Ohara R., Imamoto S., Koseki H., Hirakawa S.,  
 Suga Y., Kitanura H., Nakagawa T., Nagase T., Ohara O., Koga H.,  
 "Prediction of the Coding Sequences of Mouse Homologues of FLD Genes:  
 The Complete Nucleotide Sequences of 110 Mouse FLD-Homologous cDNAs  
 Identified by Screening of Terminal Sequences of cDNA Clones Randomly  
 Sampled from Size-Fractionated Libraries.";  
 DNA Res. 11:167-180(2004).  
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DR EMBL: AK131140; BMD21390.1; -.  
 DR MGI: MGI:1918996; Rg13.  
 DR GO: GO:0005515; F:Protein binding; IPI.  
 DR GO: GO:0008321; F:Rat guanyl-nucleotide exchange factor activity; IDA.  
 DR GO: GO:0017016; F:Ras GTPase binding; IDA.  
 DR GO: GO:0007218; P:neuropeptide signaling pathway; RCA.  
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; TAS.  
 DR InterPro: IPR001895; RasGRF\_CDC25.  
 DR InterPro: IPR001895; RasGEF\_CDC25.  
 DR Pfam: PF00788; RA; 1.  
 DR Pfam: PF00617; RasGEF\_1.  
 DR SMART: SM00147; RasGEF\_1.  
 DR PROSITE: PS50200; RA; 1.  
 DR PROSITE: PS00720; RasGEF\_1.  
 DR PROSITE: PS50009; RasGEF\_CAT, 1.  
 FT NON TER 1 1  
 FT NON TER 505 505  
 SQ SEQUENCE 505 AA; 55486 MW; 85333D2A74ED0CA1 CRC64;  
 QY 325 EKWIRIAORCRELRNPSLRATLSALOSNPYRLKRSWGAVSREPLS 371  
 DB 147 EKWIRIAORCRELRNPSLRATLSALOSNPYRLKRSWGAVSREPLS 193  
 RESULT 5  
 ID Q8BKD3\_MOUSE PRELIMINARY; PRT; 687 AA.  
 AC Q8BKD3;  
 DT 01-MAR-2003, integrated into UniProtKB/TrEMBL.  
 DT 01-MAR-2003, sequence version 1.  
 DT 07-FEB-2006, entry version 20.  
 DE 0 day neonate eyeball cDNA, RIKEN full-length enriched library,  
 DE clone:EI30107816 product:RALGDS-RELATED EFFECTOR PROTEIN OF M-RAS,  
 DE full insert sequence.  
 GN Name=Rg13;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridae; Muridae; Murinae; Mus.  
 NCBI\_TaxId=10090;  
 RN NUCLEOTIDE SEQUENCE.  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=Eyeball;  
 RC PubMed:16141072; DOI=10.1126/science.1112014;  
 RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
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 Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 Banal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
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 Di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,  
 Fletcher C.F., Fukushima T., Furuno M., Fukui S., Gariboldi M.,  
 Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
 Gustincich S., Harbers M., Hayashizaki Y., Hensch T.K., Hirokawa N.,  
 Hill D., Hummelbeck L., Iacono M., Ikeo K., Imae A., Ishikawa T.,  
 Jaki M., Kanapin A., Katoh M., Kawasawa Y., Kelso J., Kitamura H.,  
 Kitano H., Kollias G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,









RN NUCLEOTIDE SEQUENCE.  
 RP MEDLINE=20418060; PubMed=10869344;  
 RA Shao H., Andres D.A.;  
 RT "A novel RalGEF-like protein, RGL3, as a candidate effector for rit  
 J. Biol. Chem. 275:26914-26924(2000)."  
 RL  
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 CC  
 CC EMBL: AF237669; AAF78208.1; -; mRNA.  
 DR HSSP: O61193; 1RLF.  
 DR Ensembl: ENSMUSG00000040146; Mus musculus.  
 DR MGI: MG1:191896; Rg13.  
 DR GO: GO:0005515; F:protein binding; IPL.  
 DR GO: GO:0008321; F:Rai guanyl-nucleotide exchange factor activity; IDA.  
 DR GO: GO:0017216; P:Ras GTPase binding; IDA.  
 DR GO: GO:0007218; P:neuropeptide signaling pathway; RCA.  
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; RCA.  
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; TAS.  
 DR InterPro: IPR000159; RA.  
 DR InterPro: IPR000551; Rasgef.N.  
 DR InterPro: IPR001895; RasGRF\_CDC25.  
 DR Pfam: PF00788; RA; 1.  
 DR Pfam: PF00617; RasGEF; 1.  
 DR Pfam: PF00618; RasGEF\_N; 1.  
 DR SMART: SM00314; RA; 1.  
 DR SMART: SM00147; RasGEFN; 1.  
 DR SMART: SM00229; RasGEFN; 1.  
 DR PROSITE: PS0200; RA; 1.  
 DR PROSITE: PS00720; RasGEF; 1.  
 DR PROSITE: PS50009; RasGEF\_CAT; 1.  
 DR PROSITE: PS50212; RasGEF\_NTER; 1.  
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 SQ SEQUENCE 709 AA; 77973 MW; 607CAFE13BA609 CRC64;  
  
 Query Match 6.6%; Score 47; DB 2; Length 709;  
 Best Local Similarity 100.0%; Pred.No. 2.3e-35;  
 Matches 47; Conservative 0; Mismatches 0; Indels 0; Gaps 0.  
  
 QY 325 EKWIRIAQRCRELRNFSSILRALISALOSNPRIYLKRSWAVSREPPL 371  
 Db 326 EKWIRIAQRCRELRNFSSILRALISALOSNPRIYLKRSWAVSREPPL 372  
  
 RESULT 9  
 QSTVUG\_HUMAN  
 ID QSTVUG\_HUMAN PRELIMINARY; PRT; 309 AA.  
 AC QSTVUG.  
 DT 21-DEC-2004, integrated into UniProtKB/TrEMBL.  
 DT 21-DEC-2004, sequence version 1.  
 DT 07-FEB-2006, entry version 7.  
 DE Rai guanine nucleotide dissociation stimulator (Fragment).  
 GN Name=RAGDS; ORFNames=Rp11-326I24.1-010,  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;  
 OC Homo.  
 NCBI\_TaxID=9606;  
 RX  
 RN NUCLEOTIDE SEQUENCE.  
 RA Kimberley A.;  
 RL Submitted (May-2005) to the EMBL/GenBank/DBSJ databases.  
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 CC  
 CC EMBL: AL162417; CA113414.1; -; Genomic DNA.  
 DR Ensembl: ENSG00000160271; Homo sapiens.  
 DR GO: GO:0005085; F:guanylyl-nucleotide exchange factor activity; IEA.  
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.  
 DR InterPro: IPR001895; RasGRF\_CDC25.  
 DR Pfam: PF00617; RasGEF; 1.

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DR SMART; SMO0147; RASGEF; 1.
DR PROSITE; PS00720; RASGEF; 1.
DR PROSITE; PS50009; RASGEF_CAT; 1.
FT NON_TER 1 1
FT NON_TER 309 1
SQ SEQUENCE 309 AA; 34707 MW; 41CFPF7A9DA4A9B CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 6.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy 421 VPLYGTFPLDVLMDTA 437
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124 VPLYGTFPLDVLMDTA 140

RESULT 10
Q8N4Y1_HUMAN PRELIMINARY; PRT; 411 AA.
AC Q8N4Y1;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 15.
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
DR EMBL; BC03198; AAH3198.1; -; mRNA.
DR HSSP; Q12967; 2RGF.
DR Ensemble; ENSG00000160271; Homo sapiens.
DR GO; GO:0005085; F:guanylyl-nucleotide exchange factor activity; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR00159; RA.
DR Pfam; PF00788; RA; 1.
DR Pfam; PF00617; RASGEF; 1.
DR SMART; SMO0314; RA; 1.
DR PROSITE; PS50200; RA; 1.
DR PROSITE; PS00720; RASGEF; 1.
DR PROSITE; PS50009; RASGEF_CAT; 1.
DR Hypothetical protein.
KW NON_TER 1
FT NON_TER 1
SQ SEQUENCE 411 AA; 45526 MW; 11AC1F26F923B79 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 8.9e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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124 VPLYGTFPLDVLMDTA 77

RESULT 11
Q3UEA9_MOUSE PRELIMINARY; PRT; 555 AA.
AC Q3UEA9;
DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.
DT 11-OCT-2005, sequence version 1.
DT 07-FEB-2006, entry version 5.
DE Bone marrow macrophage cDNA, RIKEN full-length enriched library,

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DE clone:G530007E09 product:rat guanine nucleotide dissociation  
stimulator, full insert sequence. (Fragment).  
GN Name:RatGds.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
NCBI\_TaxId=10090;  
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NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
RA Carninci P., Hayashizaki Y.;  
RT "High-efficiency full-length cDNA cloning.";  
RL Methods Enzymol. 303:19-44(1999).  
[2]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX PubMed=16141072; DOI=10.1126/science.1112014;  
RA Carninci P., Kasukawa T., Katayama S., Gough J., Frith M.C., Maeda N.,  
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Davis M.J., Wilm M., Wang L.G., Aldins E., Allen J.E.,  
Ambesi-Impombato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
Banal M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
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di Bernardo D., Down T., Engstrom P., Fagiolini M., Faulkner G.,  
Fleischer C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,  
Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
Hill D., Hummelbeck L., Iacono M., Ikeo K., Iwama A., Ishikawa T.,  
Jakt M., Kanapin A., Katoh M., Kawasawa Y., Kello J., Kitamura H.,  
Kitano H., Kollis G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
Liu S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
Mottason R., Nishiguchi S., Nishikawa S., Noi F., Ohtsuka T.,  
Okazaki Y., Oriando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,  
Petrovsky N., Piazza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
Roest B., Ruan Y., Salzberg S.L., Sandelin A., Schneider C.,  
Schonbach C., Sekiguchi K., Sempile C.A., Sessa L., Sheng Y.,  
Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
Sperling S., Stupka E., Sugtara K., Sultana R., Takenawa T., Taki K.,  
Tamada K., Tan S.L., Tang S., Taylor W.S., Tegler J., Teichmann S.A.,  
Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yang K.,  
Yamanishi H., Zdobych E., Zhu S., Zimmer A., Hide W., Bult C.,  
Grimmond S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
Wahlestedt C., Mattick J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arikawa T.,  
Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
Kawashima T., Kojima M., Kondo S., Kono H., Nakano K., Nimoto N.,  
Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,  
Hayashizaki Y.;  
RT "The transcriptional landscape of the mammalian genome.";  
RL Science 309:1559-1563(2005).  
[3]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX PubMed=16141073; DOI=10.1126/science.1112009;  
RG RIKEN Genome Exploration Research Group and Genome Science Group  
(Genome Network Core Team) and the FANTOM Consortium;  
RT "Antisense transcription in the Mammalian Transcriptome.";  
RL Science 309:1564-1566(2005).  
[4]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX MEDLINE=22356883; PubMed=1466851; DOI=10.1038/nature01266;  
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,  
Nikaido I., Otsu N., Saito R., Suzuki H., Yamada I., Kiyosawa H.,  
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,  
BALDARELLI R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,  
Blake J.A., Bradt D., Brusic V., Chothia C., Cobani L.E., Cousins S.,  
Dalla E., Dragani T.A., Fletcher C.F., Forrest A.R., Fraser K.S.,  
GAESTERLAND T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
R. GRIMMOND S., Gustincich S., Hirokawa N., Jankovic I., Jarvis E.D.,  
Kana A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
Kongaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
Maggioli D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G.,  
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramchandran S.,  
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
Sandalin A., Schneider C., Sempile C.A., Setou R., Shimada K.,  
Sultana R., Takenawa T., Taylor M.S., Teasdale R.D., Tomita K.,  
Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
Wilm M., Wilmshaw-Boris A., Yanagisawa M., Yang I., Yang L.,  
Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayashizaki Y.,  
Hirokawa N., Kishikawa T., Kono H., Nakamura M., Sakazume N.,  
Shiraki T., Waki K., Kawai J., Aizawa K., Arikawa T., Fukuda S.,  
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
[5]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,  
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
Fleischmann W., Gaesteland T., Gissi C., King B., Kochia H.,  
Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamliya M., Lee N.H.,  
Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,  
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Sasaki H., Sato K., Schonbach C., Seta T., Shibata Y., Storch K.-F.,  
Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilm M.,  
Wilmshaw-Boris A., Yoshida K., Hasegawa Y., Kawai J., Kohsaki S.,  
Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[6]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,  
Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subcloning of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[7]  
NP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;  
RX MEDLINE=22356883; PubMed=1466851; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagoka S., Sasaki N., Carninci P.,  
Kono H., Akiyama J., Nishi K., Kiyosawa T., Tashiro H., Itoh M.,  
Sun H., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe K.,  
Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuda S., Kawai J.,  
Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).

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RN [8]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=Bone marrow;
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,
RA Hori F., Iida J., Imamura K., Imciani K., Itoh M., Kanagawa S.,
RA Kawai J., Kojima M., Kono H., Murata M., Nakamura M., Nishimura N.,
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Watanabe A.,
RA Muramatsu M., Hayashizaki Y.;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AK149644; BAE2902.1; -; mRNA.
DR MGI; MGI:107485; Ralsgds.
DR GO; GO:0008289; F:lipid binding; RCA.
DR GO; GO:0005515; F:protein binding; IPI.
DR GO; GO:0006810; P:transport; RCA.
DR InterPro; IPR001895; RasGRF_CDC25.
DR Pfam; PF00788; RA; 1.
DR SMART; SM00617; RasGEF; 1.
DR SMART; SM00147; RasGEF; 1.
DR PROSITE; PS50200; RA; 1.
DR PROSITE; PS00720; RasGEF; 1.
DR PROSITE; PS50009; RasGEF_CAT; 1.
DR NON TER 1 1
SQ SEQUENCE 555 AA; 62049 MW; 8F2ACB72F59BD04B CRC64;

Query Match 2.4%; Score 17; DB 2; Length 555;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 421 VPIYGTFLTDVWMLDTA 437
DB 205 VPIYGTFLTDVWMLDTA 221

RESULT 12
O8NF31_HUMAN PRELIMINARY; PRT; 625 AA.
AC O8NF31;
DT 01-OCT-2002, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2002, sequence version 1.
DT 07-FEB-2006, entry version 12.
DE FLJ00371 protein (Fragment).
GN Name=FLJ00371;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Spleen;
RA Jikuya H., Takano J., Kikuno R., Nagase T., Ohara O.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
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CC -----
CC EMBL; AK090450; BAC03431.1; -; mRNA.
DR HSSP; Q12967; 2RGF.
DR Ensemble; ENSG00000160271; Homo sapiens.
DR GO; GO:0005085; F:guanylate-kinase exchange factor activity; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR001895; RasGRF_CDC25.
DR Pfam; PF00617; RasGEF; 1.
DR SMART; SM00147; RasGEF; 1.
DR PROSITE; PS00720; RasGEF; 1.
DR PROSITE; PS50009; RasGEF_CAT; 1.
DR NON TER 1 1
SQ SEQUENCE 745 AA; 81765 MW; 3A2330D768BE6E7D CRC64;

Query Match 2.4%; Score 17; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 421 VPIYGTFLTDVWMLDTA 437
DB 360 VPIYGTFLTDVWMLDTA 376

RESULT 14
O8TEK9_HUMAN PRELIMINARY; PRT; 824 AA.
AC O8TEK9;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE FLJ00185 protein (Fragment).
GN Name=FLJ00185;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;

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FT NON TER 1 1
SQ SEQUENCE 625 AA; 68192 MW; 9FFC16C867F54561 CRC64;

Query Match 2.4%; Score 17; DB 2; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.3e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 421 VPIYGTFLTDVWMLDTA 437
DB 353 VPIYGTFLTDVWMLDTA 369

RESULT 13
O9P2N8_HUMAN PRELIMINARY; PRT; 745 AA.
AC O9P2N8;
DT 01-OCT-2000, integrated into UniProtKB/TrEMBL.
DT 01-OCT-2000, sequence version 1.
DT 07-FEB-2006, entry version 17.
DE KIAA1308 protein (Fragment).
GN Name=KIAA1308;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=20181126; PubMed=10718198; DOI=10.1093/dnares/7.1.65;
RA Nagase T., Kikuno R., Ishikawa K., Hirosewa M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVI.
RT The complete sequences of 150 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 7:65-73(2000).
CC -----
CC Copyrighted by the UniProt Consortium, see http://www.uniprot.org/terms
CC Distributed under the Creative Commons Attribution-NonDerivs license
CC -----
CC EMBL; AB037729; BAA92546.1; -; mRNA.
DR GO; GO:0005085; F:guanylate-kinase exchange factor activity; IEA.
DR GO; GO:0007264; P:small GTPase mediated signal transduction; IEA.
DR InterPro; IPR001895; RasGRF_CDC25.
DR Pfam; PF00617; RasGEF; 1.
DR SMART; SM00147; RasGEF; 1.
DR PROSITE; PS00720; RasGEF; 1.
DR PROSITE; PS50009; RasGEF_CAT; 1.
DR NON TER 1 1
SQ SEQUENCE 745 AA; 81765 MW; 3A2330D768BE6E7D CRC64;

Query Match 2.4%; Score 17; DB 2; Length 745;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 421 VPIYGTFLTDVWMLDTA 437
DB 360 VPIYGTFLTDVWMLDTA 376

RESULT 14
O8TEK9_HUMAN PRELIMINARY; PRT; 824 AA.
AC O8TEK9;
DT 01-JUN-2002, integrated into UniProtKB/TrEMBL.
DT 01-JUN-2002, sequence version 1.
DT 07-FEB-2006, entry version 14.
DE FLJ00185 protein (Fragment).
GN Name=FLJ00185;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;

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RN [1]  
 RC NUCLEOTIDE SEQUENCE.  
 RA Tissue-Spleen:  
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.  
 CC -----  
 CC Copied under the Uniprot Consortium, see <http://www.uniprot.org/terms>  
 CC Distributed under the Creative Commons Attribution-NonDerivs license  
 CC -----  
 DR EMBL: AK074114; BAB84940.1; -; mRNA.  
 DR HSP; Q12967; 2RGF.  
 DR Ensembl: ENSG00000160271; Homo sapiens.  
 DR GO: GO:0005085; P:guanylyl-nucleotide exchange factor activity; IEA.  
 DR GO: GO:0007264; P:small GTPase mediated signal transduction; IEA.  
 DR InterPro: IPR000651; Rasgef N.  
 DR InterPro: IPR001895; RasGRF\_CDC25.  
 DR Pfam: PF00617; Rasgef; 1.  
 DR Pfam: PF00618; Rasgef; 1.  
 DR SMART: SM00147; Rasgef; 1.  
 DR SMART: SM00229; Rasgef; 1.  
 DR PROSITE: PS00720; Rasgef; 1.  
 DR PROSITE: PS00009; Rasgef; 1.  
 DR PROSITE: PS00212; Rasgef; 1.  
 DR NON\_TER 1  
 FT 1  
 SO SEQUENCE 824 AA; 90263 MW; EFBB582CADF8FA26 CRC64;  
 Query Match 2.4%; Score 17; DB 2; Length 824;  
 Best Local Similarity 100.0%; Pred.No.16e-06;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 421 VPTGTFITDVLMDTA 437  
 Db 552 VPTGTFITDVLMDTA 568  
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 |||||

RESULT 15  
 Q3UQY9 MOUSE PRELIMINARY; PRT; 840 AA.  
 ID Q3UQY9  
 AC Q3UQY9  
 DT 11-OCT-2005, integrated into UniProtKB/TrEMBL.  
 DT 11-OCT-2005, sequence version 1.  
 DT 07-FEB-2006, entry version 5.  
 DE 12 days embryo spinal ganglion cDNA, RIKEN full-length enriched  
 DE library, clone:DJ3075H07 product:rat guanine nucleotide dissociation  
 DE stimulator; full insert sequence.  
 GN Name=Ralgds;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
 OC Muridea; Muridae; Murinae; Mus.  
 OC NCBI\_TaxId=10090;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=spinal ganglion;  
 RX MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;  
 RA Carinini P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning";  
 RL Methods Enzymol. 303:19-44(1999).  
 RN [2]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=spinal ganglion;  
 RX PubMed=16141072; DOI=10.1126/science.1112014;  
 RA Carinini P., Kasukawa T., Katayama S., Gough J., Fitch M.C., Maeda N.,  
 RA Oyama R., Ravasi T., Lenhard B., Wells C., Kodzhus R., Shimokawa K.,  
 RA Baisic V.B., Brenner S.E., Batilov S., Forrest A.R., Zavolan M.,  
 RA Davis M.J., Wilming L.G., Aldinis V., Allen J.E.,  
 RA Amemiya-Impomatato A., Apweiler R., Aturaliya R.N., Bailey T.L.,  
 RA Banerji M., Baxter L., Beisel K.W., Bersano T., Bono H., Chalk A.M.,  
 RA Chiu K.P., Choudhary V., Christoffels A., Clutterbuck D.R.,  
 RA Crowe M.L., Dalla E., Dalrymple B.P., de Bono B., Della Gatta G.,  
 RA di Bernardo D., Down T., Engstrom P., Fagioli M., Faulkner G.,  
 RA Fletcher C.F., Fukushima T., Furuno M., Futaki S., Gariboldi M.,  
 RA Georgii-Hemming P., Gingeras T.R., Gojobori T., Green R.E.,

RA Gustincich S., Harbers M., Hayashi Y., Hensch T.K., Hirokawa N.,  
 RA Hill D., Hummelbeck L., Iacono M., Ieko K., Iwama A., Ishikawa T.,  
 RA Jaki M., Kanamori A., Katoh M., Kawasawa Y., Keiso Y., Kitamura H.,  
 RA Kitano H., Kollins G., Krishnan S.P., Kruger A., Kummerfeld S.K.,  
 RA Kurochkin I.V., Lareau L.F., Lazarevic D., Lipovich L., Liu J.,  
 RA Liuni S., McWilliam S., Madan Babu M., Madera M., Marchionni L.,  
 RA Matsuda H., Matsuzawa S., Miki H., Mignone F., Miyake S., Morris K.,  
 RA Motagani-Tabar S., Mulder N., Nakano N., Nakachi H., Ng P.,  
 RA Nilsson R., Nishiguchi S., Nishikawa S., Nori F., Ohara O.,  
 RA Okazaki Y., Orlando V., Pang K.C., Pavan W.J., Pavoni G., Pesole G.,  
 RA Petrovsky N., Plaza S., Reed J., Reid J.F., Ring B.Z., Ringwald M.,  
 RA Roost B., Ruan Y., Salzberg S.L., Sardinia A., Schneider C.,  
 RA Schonbach C., Sekiguchi K., Semple C.A., Sento S., Sessa L., Sheng Y.,  
 RA Shibata Y., Shimada H., Shimada K., Silva D., Sinclair B.,  
 RA Sperling S., Stupka E., Sugiyama K., Sultana R., Takenaka Y., Taki K.,  
 RA Tamajima K., Tan S.L., Tang S., Taylor M.S., Tegner J., Teichmann S.A.,  
 RA Ueda H.R., van Nimwegen E., Verardo R., Wei C.L., Yagi K.,  
 RA Yamashita H., Zaslavsky E., Zhu S., Zimmer A., Hide W., Bult C.,  
 RA Gilmont S.M., Teasdale R.D., Liu E.T., Brusic V., Quackenbush J.,  
 RA Wahlestedt C., Matlock J.S., Hume D.A., Kai C., Sasaki D., Tomaru Y.,  
 RA Fukuda S., Kanamori-Katayama M., Suzuki M., Aoki J., Arakawa T.,  
 RA Iida J., Imamura K., Itoh M., Kato T., Kawaji H., Kawagashira N.,  
 RA Kawashima T., Kojima M., Kondo S., Konno H., Nakano K., Niimura N.,  
 RA Nishio T., Okada M., Plessey C., Shibata K., Shiraki T., Suzuki S.,  
 RA Tagami M., Waki K., Watanabe A., Okamura-Oho Y., Suzuki H., Kawai J.,  
 RA Hayashizaki Y.;  
 RT "The transcriptional landscape of the mammalian genome";  
 RL Science 309:1559-1563(2005).  
 RN [3]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=spinal ganglion;  
 RX PubMed=16141073; DOI=10.1126/science.1112009;  
 RA RIKEN Genome Exploration Research Group, and Genome Science Group  
 RG (Genome Network Core Team) and the RANTOM Consortium;  
 RT "Antisense transcription in the mammalian transcriptome";  
 RL Science 309:1564-1566(2005).  
 RN [4]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=spinal ganglion;  
 RX MEDLINE=22554683; PubMed=12466851; DOI=10.1038/nature01266;  
 RA Okazaki Y., Furuno M., Kasukawa T., Adachi U., Bono H., Kondo S.,  
 RA Nakai I., Osato N., Saito R., Suzuki H., Yamana H., Kiyosawa H.,  
 RA Yagi K., Tomaru Y., Haegawa Y., Nogami A., Schonbach C., Gojobori T.,  
 RA Balarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,  
 RA Schriml L.M., Kanamori A., Matsuda H., Batilov S., Beisel K.W.,  
 RA Blake J.A., Brad D., Brusic V., Chochia C., Corbani L.E., Cousins S.,  
 RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,  
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,  
 RA Gilmont S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,  
 RA Kanai A., Kawai H., Kawasawa Y., Kedzierski R.M., King B.L.,  
 RA Kongsaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
 RA Nagashima T., Nunnata K., Okita T., Pavan W.J., Petosa G.,  
 RA Petrovsky N., Nunnata K., Pontius J.U., Qi D., Ramchandran S.,  
 RA Ravasi T., Reed J.C., Reed J., Reid J., Ring B.Z., Ringwald M.,  
 RA Sanderlin A., Schneider C., Semple C.A., Serou M., Shimada K.,  
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
 RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
 RA Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang L., Yang L.,  
 RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carinini P., Hayatsu N.,  
 RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shingawa A.,  
 RA Yasunishi A., Yoshino Y., Waterston R., Lander E.S., Rogers J.,  
 RA Birney E., Hayashizaki Y.;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [5]  
 RP NUCLEOTIDE SEQUENCE.  
 RC STRAIN=C57BL/6J; TISSUE=spinal ganglion;  
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kanakawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,  
RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schiraldi L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Mashio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombereys P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohetsuki S.,  
RA Hayaishizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
[6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayaishizaki Y.,  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
[7]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RX MEDLINE=20530913; PubMed=11076863; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagasaka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuana T., Tashiro H., Itoh M.,  
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Wataniki M.,  
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayaishizaki Y.,  
RT "RIKEN Integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
[8]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Spinal ganglion;  
RA Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K.,  
RA Horii F., Iida J., Imamura K., Imotani K., Itoh M., Kanagawa S.,  
RA Kawai J., Kojima M., Konno H., Murata M., Nakamura M., Ninomiya N.,  
RA Nishiyori H., Nomura K., Ohno M., Sakazume N., Sano H., Sasaki D.,  
RA Shibata K., Shiraki T., Tagami M., Tagami Y., Waki K., Wataniki A.,  
RA Muramatsu M., Hayaishizaki Y.,  
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.  
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CC Distributed under the Creative Commons Attribution-NonDerivs license  
CC  
CC EMBL: AK141959; BA24899.1; -; mRNA.  
DR MGI: MGI:107485; RA1908.  
DR GO: GO:0008289; F:lipid binding; RCA.  
DR GO: GO:0005515; F:protein binding; IPI.  
DR GO: GO:0006810; P:transport; RCA.  
DR InterPro: IPR000159; RA.  
DR InterPro: IPR000651; Rasgef N.  
DR InterPro: IPR001895; Rasgef CDC25.  
DR Pfam: PF00788; RA; 1.  
DR Pfam: PF00617; Rasgef; 1.  
DR Pfam: PF00618; Rasgef N; 1.  
DR SMART: SM00314; RA; 1.  
DR SMART: SM00147; Rasgef; 1.  
DR SMART: SM00229; Rasgef N; 1.  
DR PROSITE: PS50200; RA; 1.  
DR PROSITE: PS00720; Rasgef; 1.

DR PROSITE: PS50009; Rasgef CAT; 1.  
DR PROSITE: PS50212; Rasgef NTER; 1.  
SQ SEQUENCE 840 AA; 92920 MW; E0A0FBAB495B2A77 CRC64;  
Query Match 2.4%; Score 17; DB 2; Length 840;  
Best Local Similarity 100.0%; Pred. No. 1.7e-06;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 421 VPTLGTFLTDVLMVLDTA 437  
DB 490 VPTLGTFLTDVLMVLDTA 506

Search completed: June 12, 2006, 12:04:38  
Job time : 308 secs

GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 12, 2006, 11:59:50 ; Search time 44 Seconds  
(without alignments)  
1552.589 Million cell updates/sec

Title: US-10-694-438-2

Perfect score: 710

Sequence: 1 MERTAGKELALAPLDWGEE.....RDFMLRKEGTRNTLSVPS 710

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 1

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 80.\*

1: .pir1.\*

2: .pir2.\*

3: .pir3.\*

4: .pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID     | Description        |
|------------|-------|-------------|--------|--------|--------------------|
| 1          | 17    | 2.4         | 852    | S28415 | guanine nucleotide |
| 2          | 11    | 1.5         | 754    | T12453 | hypothetical prote |
| 3          | 11    | 1.5         | 768    | A56234 | ral guanine nucleo |
| 4          | 10    | 1.4         | 328    | I38853 | guanine nucleotide |
| 5          | 10    | 1.4         | 842    | T16198 | hypothetical prote |
| 6          | 9     | 1.3         | 94     | PC4379 | Rif. RalGDS-like f |
| 7          | 9     | 1.3         | 132    | H96708 | hypothetical prote |
| 8          | 9     | 1.3         | 150    | C85799 | dATP pyrophospho   |
| 9          | 9     | 1.3         | 150    | G90950 | dATP pyrophospho   |
| 10         | 9     | 1.3         | 150    | B38113 | dATP pyrophospho   |
| 11         | 9     | 1.3         | 438    | AF0068 | UDP-N-acetylmuram  |
| 12         | 9     | 1.3         | 502    | A55197 | Wiskott-Aldrich sy |
| 13         | 9     | 1.3         | 777    | T08659 | ral guanine nucleo |
| 14         | 9     | 1.3         | 2048   | ZLNZSE | genome polyprotein |
| 15         | 9     | 1.3         | 2828   | ZLNZSV | genome polyprotein |
| 16         | 8     | 1.1         | 152    | A83574 | hypothetical prote |
| 17         | 8     | 1.1         | 192    | T30477 | hypothetical prote |
| 18         | 8     | 1.1         | 232    | C82774 | DNA repair protein |
| 19         | 8     | 1.1         | 248    | TVMVR5 | transforming prote |
| 20         | 8     | 1.1         | 288    | T12462 | hypothetical prote |
| 21         | 8     | 1.1         | 305    | A97554 | DNA repair protein |
| 22         | 8     | 1.1         | 379    | T19069 | hypothetical prote |
| 23         | 8     | 1.1         | 388    | JC5437 | spliceosome-associ |
| 24         | 8     | 1.1         | 446    | T24958 | hypothetical prote |
| 25         | 8     | 1.1         | 449    | J01438 | polyprotein - tuli |
| 26         | 8     | 1.1         | 550    | G70597 | probable proteinas |
| 27         | 8     | 1.1         | 611    | S62811 | oligoendopeptidase |
| 28         | 8     | 1.1         | 627    | H86180 | hypothetical prote |
| 29         | 8     | 1.1         | 632    | S38042 | probable purine nu |

|    |   |     |      |   |        |                    |
|----|---|-----|------|---|--------|--------------------|
| 30 | 8 | 1.1 | 644  | 2 | T33132 | hypothetical prote |
| 31 | 8 | 1.1 | 696  | 2 | AI2849 | GGDEF family prote |
| 32 | 8 | 1.1 | 696  | 2 | G97626 | hypothetical prote |
| 33 | 8 | 1.1 | 753  | 2 | B36268 | platelet glycoprot |
| 34 | 8 | 1.1 | 778  | 2 | A60798 | platelet glycoprot |
| 35 | 8 | 1.1 | 788  | 2 | A26547 | platelet glycoprot |
| 36 | 8 | 1.1 | 788  | 2 | I77349 | platelet glycoprot |
| 37 | 8 | 1.1 | 797  | 2 | S53590 | hypothetical prote |
| 38 | 8 | 1.1 | 851  | 2 | T47305 | hypothetical prote |
| 39 | 8 | 1.1 | 909  | 2 | S32538 | cGMP-gated cation  |
| 40 | 8 | 1.1 | 1002 | 2 | I56963 | transposase - Esch |
| 41 | 8 | 1.1 | 1018 | 2 | FC4211 | neural adhesion pr |
| 42 | 8 | 1.1 | 1039 | 2 | F71427 | hypothetical prote |
| 43 | 8 | 1.1 | 1144 | 2 | T25765 | hypothetical prote |
| 44 | 8 | 1.1 | 1201 | 2 | A57369 | anillin - fruit fl |
| 45 | 8 | 1.1 | 1329 | 2 | E70917 | hypothetical glyci |

ALIGNMENTS

RESULT 1

S28415  
guanine nucleotide dissociation stimulator ralGDS - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004  
A:Accession: S28415  
R:Albright, C.F.; Giddings, B.W.; Liu, J.; Vito, M.; Weinberg, R.A.  
EMBO J. 12, 339-347, 1993  
A:Title: Characterization of a guanine nucleotide dissociation stimulator for a ras-rel  
A:Reference number: S28415; MUID:93154339; PMID:8094051  
A:Accession: S28415  
A>Status: not compared with conceptual translation  
A:Molecule type: mRNA  
A:Residues: 1-852 <ALB>  
A:Cross-references: UNIPROT:Q03385; UNIPARC:UPI0000029858; GB:L07924; NID:9193572; PIDN  
F:320-586/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match 2.4%; Score 17; DB 2; Length 852;  
Best Local Similarity 100.0%; Pred. No. 9.28-08;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 421 VPYLGTFLTDLVMLDTA 437  
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Db 502 VPYLGTFLTDLVMLDTA 518

RESULT 2

T12453  
hypothetical protein DKFZp564D2123.1 - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 23-Jul-1999 #sequence\_revision 23-Jul-1999 #text\_change 09-Jul-2004  
R:Wambutt, R.; Heubner, D.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
submitted to the Protein Sequence Database, June 1999  
A:Reference number: Z17524  
A:Accession: T12453  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-754 <WAM>  
A:Cross-references: UNIPROT:Q9NZL6; UNIPARC:UPI000016AC59; EMBL:AL080117  
A:Experimental source: fetal brain; clone DKFZp564D2123  
C:Genetics:  
A>Note: DKFZp564D2123.1  
F:1214-487/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match 1.5%; Score 11; DB 2; Length 754;  
Best Local Similarity 100.0%; Pred. No. 0.061;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 421 VPYLGTFLTDL 431  
|||  
Db 403 VPYLGTFLTDL 413

## RESULT 3

A56234  
 ral guanine nucleotide dissociation stimulator-like protein RGL - mouse  
 C/Species: Mus musculus (house mouse)  
 C/Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004  
 C/Accession: A56234  
 R/Kikuchi, A.; Demo, S.D.; Ye, Z.H.; Chen, Y.W.; Williams, L.T.  
 Mol. Cell. Biol. 14, 7483-7491, 1994  
 A/Title: ralGDS family members interact with the effector loop of ras p21.  
 A/Reference number: A56234; MUID:95021278; PMID:7935463  
 A/Accession: A56234  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-768 <K>  
 A/Cross-references: UNIPROT:Q60695; UNIPARC:UPI000002822E; GB:U14103; NID:9537276; PIDN:  
 C/Genetics:  
 A/Gene: RGL  
 F:228-501/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match 1.5%; Score 11; DB 2; Length 768;  
 Best Local Similarity 100.0%; Pred. No. 0.062;  
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 421 VPYLGTFLTDL 431  
 |||||  
 Db 417 VPYLGTFLTDL 427

## RESULT 4

I38853  
 guanine nucleotide dissociation stimulator ralGDS - human (fragment)  
 C/Species: Homo sapiens (man)  
 C/Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 09-Jul-2004  
 C/Accession: I38853  
 R/Hofer, F.; Fields, S.; Schneider, C.; Martin, G.S.  
 Proc. Natl. Acad. Sci. U.S.A. 91, 11089-11093, 1994  
 A/Title: Activated Ras interacts with the Ral guanine nucleotide dissociation stimulator  
 A/Reference number: I38853; MUID:95062211; PMID:7972015  
 A/Accession: I38853  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-328 <R>  
 A/Cross-references: UNIPROT:Q12967; UNIPARC:UPI000016A11C; EMBL:U14417; NID:9538199; PID  
 F:1-62/Domain: CDC25-type guanine nucleotide exchange activator homology (fragment) <SOS>

Query Match 1.4%; Score 10; DB 2; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 0.27;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 446 LINFEKRRKE 455  
 |||||  
 Db 3 LINFEKRRKE 12

## RESULT 5

T16198  
 hypothetical protein F28B4.2 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 09-Jul-2004  
 C/Accession: T16198  
 R/Leimbach, D.  
 submitted to the EMBL Data Library, December 1995  
 A/Description: The sequence of C. elegans cosmid F28B4.  
 A/Reference number: Z18475  
 A/Accession: T16198  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-842 <LEI>  
 A/Cross-references: UNIPROT:Q19852; UNIPARC:UPI0000017B947; EMBL:U42834; NID:g1125756; PID  
 C/Genetics:  
 A/Gene: CESP:F28B4.2

A;Introns: 17/3; 59/3; 93/2; 116/2; 229/3; 333/2; 510/2; 659/3; 738/3; 803/2  
 F;212-481/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match 1.4%; Score 10; DB 2; Length 842;  
 Best Local Similarity 100.0%; Pred. No. 0.64;  
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 446 LINFEKRRKE 455  
 |||||  
 Db 422 LINFEKRRKE 431

## RESULT 6

PC4379  
 Rlf, RalGDS-like factor - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 06-Nov-1997 #sequence\_revision 06-Nov-1997 #text\_change 07-May-1999  
 C/Accession: PC4379  
 R/O'Gara, M.J.; Zhang, X.; Baker, L.; Marshall, M.S.  
 Biochem. Biophys. Res. Commun. 238, 425-429, 1997  
 A/Title: Characterization of the Ras binding domain of the RalGDS-related protein, RLF.  
 A/Reference number: PC4379; MUID:97445998; PMID:9299525  
 A/Accession: PC4379  
 A/Status: nucleic acid sequence not shown  
 A/Molecule type: mRNA  
 A/Residues: 1-94 <OAG>  
 A/Cross-references: UNIPARC:UPI000017C73F  
 C/Comment: This protein belongs to RalGDS family which are guanine-nucleotide exchange

Query Match 1.3%; Score 9; DB 2; Length 94;  
 Best Local Similarity 100.0%; Pred. No. 0.82;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 635 TSQDKAPSV 643  
 |||||  
 Db 29 TSQDKAPSV 37

## RESULT 7

H96708  
 hypothetical protein T26J14.5 [imported] - Arabidopsis thaliana  
 C/Species: Arabidopsis thaliana (mouse-ear cress)  
 C/Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 09-Jul-2004  
 C/Accession: H96708  
 R/Theologas, A.; Ecker, J.R.; Palm, C.J.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 A/Authors: Hunter, J.L.; Lin, X.; Liu, S.X.; Luros, J.S.; Maiti, R.; Marziali  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A/Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A/Reference number: A86141; MUID:21016719; PMID:11130712  
 A/Accession: H96708  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-132 <STO>  
 A/Cross-references: UNIPROT:Q9CA33; UNIPARC:UPI00000A1CA4; GB:AE005173; NID:g6553937; P  
 C/Genetics:  
 A/Gene: T26J14.5  
 A/Map position: 1

Query Match 1.3%; Score 9; DB 2; Length 132;  
 Best Local Similarity 100.0%; Pred. No. 1.1;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 115 PMPPPPPPP 123  
 |||||  
 Db 15 PMPPPPPPP 23

## RESULT 8

CD5799  
 dATP pyrophosphohydrolase [imported] - Escherichia coli (strain O157:H7, substrain EDL93)  
 C:Species: Escherichia coli  
 C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 05-Oct-2004  
 C:Accession: CD5799  
 R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew  
 Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,  
 Nature 409, 529-533, 2001  
 A>Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
 A:Reference number: A85480; MUID:21074935; PMID:11206551  
 A:Accession: CD5799  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-150 <STO>  
 A:Cross-references: UNIPROT:P24236; UNIPARC:UPI00001308E5; GB:AE005174; NID:g12515921; F  
 A:Experimental source: strain O157:H7, substrain EDL933  
 C:Genetics:  
 A:Gene: Z2917

Query Match 1.3%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 VAEQLTLID 259

|||||

Db 66 VAEQLTLID 74

## RESULT 9

G90950  
 dATP pyrophosphohydrolase [imported] - Escherichia coli (strain O157:H7, substrain RMD  
 C:Species: Escherichia coli  
 C>Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 05-Oct-2004  
 C:Accession: G90950  
 R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
 DNA Res. 8, 11-22, 2001  
 A>Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
 A:Reference number: A99629; MUID:21156231; PMID:11358796  
 A:Accession: G90950  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-150 <HAY>  
 A:Cross-references: UNIPROT:P24236; UNIPARC:UPI00001308E5; GB:BA000007; PIDN:BA035998.1;  
 A:Experimental source: strain O157:H7, substrain RMD 050952  
 C:Genetics:  
 A:Gene: EC2575

Query Match 1.3%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 VAEQLTLID 259

|||||

Db 66 VAEQLTLID 74

## RESULT 10

B38113  
 dATP pyrophosphohydrolase (EC 3.6.1.-) - Escherichia coli (strain K-12)  
 C:Species: Escherichia coli  
 C>Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 31-Dec-2004  
 C:Accession: B38113; S19013; A64949  
 R;Takahagi, M.; Iwasaki, H.; Nakata, A.; Shinagawa, H.  
 J. Bacteriol. 173, 5747-5753, 1991  
 A>Title: Molecular analysis of the Escherichia coli ruvC gene, which encodes a Holliday  
 A:Reference number: A38113; MUID:91358366; PMID:1885548  
 A:Accession: B38113  
 A>Status: preliminary; not compared with conceptual translation  
 A:Molecule type: DNA  
 A:Residues: 1-150 <TAK>  
 A:Cross-references: UNIPROT:P24236; UNIPARC:UPI00001308E5; GB:D10165; GB:D90392; NID:g21

R;Sharples, G.J.; Lloyd, R.G.  
 J. Bacteriol. 173, 7711-7715, 1991  
 A>Title: Resolution of Holliday junctions in Escherichia coli: identification of the ru  
 A:Reference number: S19013; MUID:92041688; PMID:1657895  
 A:Accession: S19013  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-150 <SHA>  
 A:Cross-references: UNIPARC:UPI00001308E5; EMBL:X59551; NID:g42172; PIDN:CAA42124.1; PI  
 A:Experimental source: strain K-12  
 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C  
 .A.; Rose, D.J.; Mau, B.; Shao, Y.  
 Science 277, 1453-1462, 1997  
 A>Title: The complete genome sequence of Escherichia coli K-12.  
 A:Reference number: A64720; MUID:97426617; PMID:9278503  
 A:Accession: A64949  
 A>Status: nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-150 <BLAT>  
 A:Cross-references: UNIPARC:UPI00001308E5; GB:AE000280; GB:U00096; NID:g1788163; PIDN:AJ  
 A:Experimental source: strain K-12, substrain MG1655  
 C:Genetics:  
 A:Gene: ntpA  
 C:Keywords: hydrolase  
 F;36-70/Domain: mutT domain homology <MUTT>

Query Match 1.3%; Score 9; DB 2; Length 150;  
 Best Local Similarity 100.0%; Pred. No. 1.3;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 251 VAEQLTLID 259

|||||

Db 66 VAEQLTLID 74

## RESULT 11

AF0068  
 UDP-N-acetylmuramoylalanine-D-glutamate ligase (EC 6.3.2.9) [imported] - Yersinia pestis  
 C:Species: Yersinia pestis  
 C>Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 09-Jul-2004  
 C:Accession: AF0068  
 R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.  
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
 il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,  
 Nature 413, 523-527, 2001  
 A>Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
 A:Reference number: AB0001; MUID:21470413; PMID:11586360  
 A:Accession: AF0068  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-438 <KUR>  
 A:Cross-references: UNIPROT:Q8ZIF1; UNIPARC:UPI00000DC8F9; GB:AL590842; PIDN:CAC89409.1;  
 C:Genetics:  
 A:Gene: murD  
 C:Superfamily: UDP-N-acetylmuramate-alanine ligase  
 C:Keywords: ligase

Query Match 1.3%; Score 9; DB 2; Length 438;  
 Best Local Similarity 100.0%; Pred. No. 3.4;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 666 VLPQDRVLL 674

|||||

Db 402 VLPQDRVLL 410

## RESULT 12

A55197  
 Wiskott-Aldrich syndrome protein WASP - human  
 C:Species: Homo sapiens (man)  
 C>Date: 23-Mar-1995 #sequence\_revision 24-Nov-1999 #text\_change 09-Jul-2004  
 C:Accession: A54747; A55197; I38931  
 R;Derry, J.M.J.; Ochs, H.D.; Francke, U.



```
Cell 78, 635-644, 1994
A:Title: Isolation of a novel gene mutated in Wiskott-Aldrich syndrome.
A:Reference number: A54747; MUID:94349367; PMID:8069912
A:Accession: A54747
A:Molecule type: mRNA
A:Residues: 1-328, 'A', 330-366, 'LHHHPLQLLDVLDHCPLEHVGHPCHH', 'HRRHRRPAPGMDQPLPHSLLLMQ
A:Cross-references: UNIPROT:P42768; UNIPARC:UPI000017C421; GB:U12707
A>Note: this sequence is corrected in reference A55197
R:Derry, J.M.J.; Ochs, H.D.; Francke, U.
Cell 79, 922a, 1994
A:Reference number: A55197
A:Contents: erratum
A:Accession: A55197
A:Molecule type: mRNA
A:Residues: 1-424, 'PG', 427-502 <DER>
A:Cross-references: UNIPARC:UPI000017C422; GB:U12707; NID:9695150
A>Note: the translated sequence in GenBank entry HSU12707 (PIDN:AAA62663.1) differs from
R:Kwan, S.P.; Hagemann, T.L.; Radtke, B.E.; Blaese, R.M.; Rosen, F.S.
Proc. Natl. Acad. Sci. U.S.A. 92, 4706-4710, 1995
A:Title: Identification of mutations in the Wiskott-Aldrich syndrome gene and characteri
A:Reference number: I38931; MUID:95273432; PMID:7753869
A:Accession: I38931
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-502 <KWA>
A:Cross-references: UNIPARC:UPI000003CA0A; EMBL:U19927; NID:9854672; PIDN:AAC50140.1; PI
C:Genetics:
A:Gene: GDB:WAS; IMD2; WASP
A:Cross-references: GDB:120736; OMIM:301000
A:Map position: Xp11.23-Xp11.22
A>Note: defects in this gene may result in Wiskott-Aldrich syndrome
C:Keywords: immunodeficiency

Query Match 1.3%; Score 9; DB 2; Length 502;
Best Local Similarity 100.0%; Pred. No. 3.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 115 PMPMPPPPP 123
DB 391 PMPMPPPPP 399

RESULT 13
T08659
xal guanine nucleotide dissociation stimulator-like protein RGL2 - human
N:Alternate names: protein DKFZp547D0710.1; RalGDS-like factor RGL2
C:Species: Homo sapiens (man)
C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: T08659
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, May 1999
A:Reference number: Z16466
A:Accession: T08659
A:Molecule type: mRNA
A:Residues: 1-777 <POU>
A:Cross-references: UNIPROT:O15211; UNIPARC:UPI0000001621; EMBL:AL050259
A:Experimental source: fetal brain; clone DKFZp547D0710
C:Genetics:
A>Note: DKFZp547D0710.1
C:Function:
A:Description: probably involved in Ras-mediated cellular transformation
P:239-513/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>

Query Match 1.3%; Score 9; DB 2; Length 777;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 TSQDKAPSV 643
DB 671 TSQDKAPSV 679

RESULT 14
```

```
ZLNZSE
genome polyprotein - Sendai virus (strain Enders)
N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: Sendai virus
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A24293
R:Morgan, E.M.; Rakestraw, K.M.
Virology 154, 31-40, 1986
A:Title: Sequence of the Sendai virus L gene: open reading frames upstream of the main c
A:Reference number: A24293; MUID:86317720; PMID:3019006
A:Accession: A24293
A:Molecule type: genomic RNA
A:Residues: 1-2048 <MOR>
A:Cross-references: UNIPROT:P06829; UNIPARC:UPI0000134AF9; GB:M14887; NID:G334975; PIDN
C:Genetics:
A:Gene: L
C:Superfamily: parainfluenza virus RNA-directed RNA polymerase
C:Keywords: ATP; nucleotidyltransferase

Query Match 1.3%; Score 9; DB 1; Length 2048;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 DLELFKVR 267
DB 1230 DLELFKVR 1238

RESULT 15
ZLNZSV
genome polyprotein - Sendai virus (strain Z)
N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)
C:Species: Sendai virus
C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A04120
R:Shioda, T.; Iwasaki, K.; Shibuta, H.
Nucleic Acids Res. 14, 1545-1563, 1986
A:Title: Determination of the complete nucleotide sequence of the Sendai virus genome R
A:Reference number: A00878; MUID:86148492; PMID:3005975
A:Accession: A04120
A:Molecule type: genomic RNA
A:Residues: 1-2228 <SHI>
A:Cross-references: UNIPROT:P06447; UNIPARC:UPI0000134AFB; GB:X03614; NID:960898; PIDN:(
C:Genetics:
A:Gene: L
C:Superfamily: parainfluenza virus RNA-directed RNA polymerase
C:Keywords: ATP; nucleotidyltransferase

Query Match 1.3%; Score 9; DB 1; Length 2228;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 259 DLELFKVR 267
DB 1410 DLELFKVR 1418

Search completed: June 12, 2006, 12:05:27
Job time : 47 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.  
OM protein - protein search, using sw model  
Run on: June 12, 2006, 12:16:58 ; Search time 181 Seconds  
(without alignments)  
1817.031 Million cell updates/sec

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Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0  
Searched: 2097797 seqs, 463214858 residues

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Maximum DB seq length: 200000000  
Post-processing: Listing first 45 summaries

Database : Published Applications AA\_Main:  
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2: /ENC\_Celerra\_SIDS3/ptodata/2/pubpaa/US08\_PUBCOMB.pep.\*  
3: /ENC\_Celerra\_SIDS3/ptodata/2/pubpaa/US09\_PUBCOMB.pep.\*  
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5: /ENC\_Celerra\_SIDS3/ptodata/2/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /ENC\_Celerra\_SIDS3/ptodata/2/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID                  | Description        |
|------------|-------|-------------|--------|---------------------|--------------------|
| 1          | 710   | 100.0       | 710    | US-10-118-328-2     | Sequence 2, Appli  |
| 2          | 710   | 100.0       | 710    | US-10-694-438-2     | Sequence 2, Appli  |
| 3          | 609   | 85.8        | 710    | US-10-060-990-3     | Sequence 3, Appli  |
| 4          | 609   | 85.8        | 710    | US-10-287-218-9     | Sequence 9, Appli  |
| 5          | 609   | 85.8        | 710    | US-10-474-291-9     | Sequence 9, Appli  |
| 6          | 609   | 85.8        | 710    | US-10-894-680A-3    | Sequence 3, Appli  |
| 7          | 487   | 68.6        | 715    | US-09-808-701A-33   | Sequence 33, Appli |
| 8          | 487   | 68.6        | 715    | US-10-233-131-33    | Sequence 33, Appli |
| 9          | 487   | 68.6        | 715    | US-10-240-145-85    | Sequence 85, Appli |
| 10         | 487   | 68.6        | 715    | US-10-291-128-85    | Sequence 85, Appli |
| 11         | 449   | 63.2        | 699    | US-09-808-701A-34   | Sequence 34, Appli |
| 12         | 449   | 63.2        | 699    | US-10-233-131-34    | Sequence 34, Appli |
| 13         | 449   | 63.2        | 699    | US-10-240-145-86    | Sequence 86, Appli |
| 14         | 449   | 63.2        | 699    | US-10-291-128-86    | Sequence 86, Appli |
| 15         | 435   | 61.3        | 464    | US-10-094-749-2959  | Sequence 2959, Ap  |
| 16         | 381   | 53.7        | 708    | US-10-074-978A-76   | Sequence 76, Appli |
| 17         | 264   | 37.2        | 264    | US-10-894-680A-60   | Sequence 60, Appli |
| 18         | 261   | 36.8        | 261    | US-10-074-978A-336  | Sequence 336, App  |
| 19         | 211   | 29.7        | 211    | US-10-074-978A-338  | Sequence 338, App  |
| 20         | 207   | 29.2        | 208    | US-10-108-260A-3953 | Sequence 3953, Ap  |
| 21         | 100   | 14.1        | 135    | US-10-894-680A-55   | Sequence 55, Appli |
| 22         | 87    | 12.3        | 87     | US-10-894-680A-65   | Sequence 65, Appli |
| 23         | 73    | 10.3        | 75     | US-10-074-978A-344  | Sequence 344, App  |
| 24         | 56    | 7.9         | 83     | US-10-074-978A-342  | Sequence 342, App  |
| 25         | 48    | 6.8         | 70     | US-09-864-761-40158 | Sequence 40158, A  |
| 26         | 47    | 6.6         | 343    | US-10-074-978A-333  | Sequence 333, App  |
| 27         | 47    | 6.6         | 343    | US-10-074-978A-334  | Sequence 334, App  |

ALIGNMENTS

RESULT 1

US-10-118-328-2  
; Sequence 2, Application US/10118328  
; Publication No. US20020169289A1  
; GENERAL INFORMATION:  
; APPLICANT: YAN Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE  
; FILE OF INVENTION: PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CL001220  
; CURRENT APPLICATION NUMBER: US/10/118.328  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/282,460  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-118-328-2

Query Match Similarity 100.0%; Score 710; DB 4; Length 710;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MERTAGKELALAPLQDWGEEEDGAVYVSUURQRQRSPAGPGGSOAPSPIANTFLH 60  
DB 1 MERTAGKELALAPLQDWGEEEDGAVYVSUURQRQRSPAGPGGSOAPSPIANTFLH 60  
QY 61 YRTSKVRVLRARLERLVGELVFGDREQDPSFMAFLATYTFVTACLLGLFLPPMPP 120  
DB 61 YRTSKVRVLRARLERLVGELVFGDREQDPSFMAFLATYTFVTACLLGLFLPPMPP 120  
QY 121 PPGVEIKKTAVQDLSEFNKILRAVVSVLGSVLQDHPQDFRDHPVHSDLSGVRTFLGWAAP 180  
DB 121 PPGVEIKKTAVQDLSEFNKILRAVVSVLGSVLQDHPQDFRDHPVHSDLSGVRTFLGWAAP 180  
QY 181 GSAEAKAEKLLDLEAEAREEQEPPQVWTPPVRAQTSDDPSSEACAESEEGIMPGQ 240  
DB 181 GSAEAKAEKLLDLEAEAREEQEPPQVWTPPVRAQTSDDPSSEACAESEEGIMPGQ 240  
QY 241 PQLDFFSVDVAEQTLTDLLEFSKVRLYECLGSVWSQDRPAGAGASPTVRATVAQNT 300  
DB 241 PQLDFFSVDVAEQTLTDLLEFSKVRLYECLGSVWSQDRPAGAGASPTVRATVAQNT 300  
QY 301 VTGCVLGSVLGAPGLAAPQRAORLEKIRIAQRCELRFNFSRLAISALQSNPIYRLKR 360  
DB 301 VTGCVLGSVLGAPGLAAPQRAORLEKIRIAQRCELRFNFSRLAISALQSNPIYRLKR 360

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QY 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEDNTPGSLSPKPPGP 420
Db 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEDNTPGSLSPKPPGP 420
QY 421 VPYLGTFDLTDLVMDLTALPDMLDGLINFEKRRKWEILARIQOLQRCQSYTLSPHPPI 480
Db 421 VPYLGTFDLTDLVMDLTALPDMLDGLINFEKRRKWEILARIQOLQRCQSYTLSPHPPI 480
QY 481 LAALHAQNQLTEQSYRLSRVIEPPAASCPSRRIRRIISLTKLSAKLAREKSSSPSGS 540
Db 481 LAALHAQNQLTEQSYRLSRVIEPPAASCPSRRIRRIISLTKLSAKLAREKSSSPSGS 540
QY 541 PGDPSSTSVSPGSPSSPRSRDAPAGSPGPGQPGSTKPLSLDLSPRPFALPLG 600
Db 541 PGDPSSTSVSPGSPSSPRSRDAPAGSPGPGQPGSTKPLSLDLSPRPFALPLG 600
QY 601 SPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQOKAPSVVRRALQKHNVPQWACD 660
Db 601 SPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQOKAPSVVRRALQKHNVPQWACD 660
QY 661 YQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710
Db 661 YQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710

RESULT 2
US-10-694-438-2
; Sequence 2, Application US/10694438
; Publication No. US20040142352A1
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CL001220-DIV
; CURRENT APPLICATION NUMBER: US/10/694,438
; CURRENT FILING DATE: 2003-10-28
; PRIOR APPLICATION NUMBER: 10/118,328
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/282,460
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-694-438-2

Query Match 100.0%; Score 710; DB 4; Length 710;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MERTAGKELALAPLQDWGEETEGAVYSVLRQRORRSPAGPGGSOAPSPIANTFLH 60
Db 1 MERTAGKELALAPLQDWGEETEGAVYSVLRQRORRSPAGPGGSOAPSPIANTFLH 60
QY 61 YRTSKVRVLAARLERLVGELVFGDREODPSFMPAFATYRTFVPTACLLGFLLPMPPPP 120
Db 61 YRTSKVRVLAARLERLVGELVFGDREODPSFMPAFATYRTFVPTACLLGFLLPMPPPP 120
QY 121 PPPGVBIKKTAVODLSFNKNLRAVSVLGSWLQHPQDFRDHPVSDLSGSRVTFLLGWAAP 180
Db 121 PPPGVBIKKTAVODLSFNKNLRAVSVLGSWLQHPQDFRDHPVSDLSGSRVTFLLGWAAP 180
QY 181 GSAEAKAEKLLDEFTLEAEAREEERPPQVWTGPPRVAQTSDDPSSEACAEDEEGLMPQG 240
Db 181 GSAEAKAEKLLDEFTLEAEAREEERPPQVWTGPPRVAQTSDDPSSEACAEDEEGLMPQG 240
QY 241 PQLLDFSDVEABQTLIDLELSKVLRYECLGSVMSQRDRPCAAGASPTVRATVAQFNT 300
Db 241 PQLLDFSDVEABQTLIDLELSKVLRYECLGSVMSQRDRPCAAGASPTVRATVAQFNT 300
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QY 301 VTGCVLGSVLGAPGAAAPQARLEKWIRIAQRCRELRFSSRLAISALQSNPIYRLKR 360
Db 301 VTGCVLGSVLGAPGAAAPQARLEKWIRIAQRCRELRFSSRLAISALQSNPIYRLKR 360
QY 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEDNTPGSLSPKPPGP 420
Db 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSOEDNTPGSLSPKPPGP 420
QY 421 VPYLGTFDLTDLVMDLTALPDMLDGLINFEKRRKWEILARIQOLQRCQSYTLSPHPPI 480
Db 421 VPYLGTFDLTDLVMDLTALPDMLDGLINFEKRRKWEILARIQOLQRCQSYTLSPHPPI 480
QY 481 LAALHAQNQLTEQSYRLSRVIEPPAASCPSRRIRRIISLTKLSAKLAREKSSSPSGS 540
Db 481 LAALHAQNQLTEQSYRLSRVIEPPAASCPSRRIRRIISLTKLSAKLAREKSSSPSGS 540
QY 541 PGDPSSTSVSPGSPSSPRSRDAPAGSPGPGQPGSTKPLSLDLSPRPFALPLG 600
Db 541 PGDPSSTSVSPGSPSSPRSRDAPAGSPGPGQPGSTKPLSLDLSPRPFALPLG 600
QY 601 SPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQOKAPSVVRRALQKHNVPQWACD 660
Db 601 SPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQOKAPSVVRRALQKHNVPQWACD 660
QY 661 YQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710
Db 661 YQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710

RESULT 3
US-10-060-990-3
; Sequence 3, Application US/10060990
; Publication No. US20030032159A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Nguyen, Cung-Tuong
; TITLE OF INVENTION: HUMAN RALGDS-LIKE PROTEIN 3
; FILE REFERENCE: PB0176
; CURRENT APPLICATION NUMBER: US/10/060,990
; CURRENT FILING DATE: 2002-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 09/864,761
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/326,105
; PRIOR FILING DATE: 2001-09-28
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 3
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-060-990-3

Query Match 85.8%; Score 609; DB 4; Length 710;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MERTAGKELALAPLQDWGEETEGAVYSVLRQRORRSPAGPGGSOAPSPIANTFLH 60
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Db 1 MERTAGKELALAPLDQWGEETEDGAVYSVLRQRSPAEQSGQAPSIANTFLH 60
Qy 61 YRTSKVRVLAARLERLVLGDEQDQSPFAFLATYRTFTVPTACLLGFLLLPMPPP 120
Db 61 YRTSKVRVLAARLERLVLGDEQDQSPFAFLATYRTFTVPTACLLGFLLLPMPPP 120
Qy 121 PPPGVEIKKTAVQDLTFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLGSVRTFLGWAAP 180
Db 121 PPPGVEIKKTAVQDLTFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLGSVRTFLGWAAP 180
Qy 181 GSAAQAKAEKLLDEFLFEAEAREQEPPQVMTGPRVAQTSDDPSSEACAEBEGLMPOG 240
Db 181 GSAAQAKAEKLLDEFLFEAEAREQEPPQVMTGPRVAQTSDDPSSEACAEBEGLMPOG 240
Qy 241 POLLDPSVDEVAEQTLIDLELFSKVRLYECLGSVMSQDRDPGAAGASPTVATVAQFNT 300
Db 241 POLLDPSVDEVAEQTLIDLELFSKVRLYECLGSVMSQDRDPGAAGASPTVATVAQFNT 300
Qy 301 VTGCVLGSVLGAPGLAAPQRAQRLKWIARQACRELRFSSRLRALSALQSNPIYRLKR 360
Db 301 VTGCVLGSVLGAPGLAAPQRAQRLKWIARQACRELRFSSRLRALSALQSNPIYRLKR 360
Qy 361 SWGAVSREPLSTFRKLSQIFSDNNHLSGREILFQEEATEGSEEDNTPGSLPKPPGP 420
Db 361 SWGAVSREPLSTFRKLSQIFSDNNHLSGREILFQEEATEGSEEDNTPGSLPKPPGP 420
Qy 421 VPYLGTFTDLVMDLTPALPDMLGDLINFEKRWKEWELIARIQOLRRQCSYTLSPHPPI 480
Db 421 VPYLGTFTDLVMDLTPALPDMLGDLINFEKRWKEWELIARIQOLRRQCSYTLSPHPPI 480
Qy 481 LAALHAQNLTEQSYRLSRVIEPPAASCPSPRIRRRISLTKLSAKLAREKSSSPSGS 540
Db 481 LAALHAQNLTEQSYRLSRVIEPPAASCPSPRIRRRISLTKLSAKLAREKSSSPSGS 540
Qy 541 PGDPSSTSVSPGSPSPSRSDAPAGPPSPGPGSTKLPLSLDLPSPRPFPALPLG 600
Db 541 PGDPSSTSVSPGSPSPSRSDAPAGPPSPGPGSTKLPLSLDLPSPRPFPALPLG 600
Qy 601 SPRIPPLAQSSARVIRVSDNDHGNLYRSILLTSQDKAPSVVRALOKHNVQPWACD 660
Db 601 SPRIPPLAQSSARVIRVSDNDHGNLYRSILLTSQDKAPSVVRALOKHNVQPWACD 660
Qy 661 YQLFQVLPGRVLLIPDNANVFVAMSPVAPDRFMLRKEGTRNTLSVSFS 710
Db 661 YQLFQVLPGRVLLIPDNANVFVAMSPVAPDRFMLRKEGTRNTLSVSFS 710

RESULT 4
US-10-287-218-9
; Sequence 9, Application US/10287218
; Publication No. US20030198975A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: AZIMZAI, Yalda; AU-YOUNG, Janice K.
; APPLICANT: BATRA, Sajeev; BAUGHN, Mariah R.
; APPLICANT: BECHA, Shanya D.; BOROWSKY, Mark L.
; APPLICANT: BUFORD, Neil; DING, Li
; APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.
; APPLICANT: GANDHI, Ameena R.; GIETZEN, Kimberly J.
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.
; APPLICANT: HONCHELL, Cynthia D.; LAL, Preeti G.
; APPLICANT: LEE, Soo Yeun; LU, Dying Aina M.
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi
; APPLICANT: REDDY, Roopa; SANJANWALA, Madhu, M.
; APPLICANT: TANG, Y. Tom; WALIA, Narinder K.
; APPLICANT: WANG, Yu-mei, E.; WARREN, Bridget A.
; APPLICANT: XU, Yuming; YANG, Junning
; APPLICANT: YAO, Monique G.; YUE, Henry
; APPLICANT: ZEBARJADIAN, Yeganeh
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH
; FILE REFERENCE: PI-0417 USA
; CURRENT APPLICATION NUMBER: US/10/287,218
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; CURRENT FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: PCT/US02/11152
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: US 60/349,705
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: US 60/295,263
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/295,340
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: US 60/293,727
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 60/291,846
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/291,662
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: US 60/287,228
; PRIOR FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/286,820
; PRIOR FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: US 60/283,294
; PRIOR FILING DATE: 2001-04-11
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PERL Program
; SEQ ID NO 9
; LENGTH: 710
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030198975A1 6937367CD1
US-10-287-218-9
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Query Match 85.8%; Score 609; DB 4; Length 710;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MERTAGKELALAPLDQWGEETEDGAVYSVLRQRSPAEQSGQAPSIANTFLH 60
Db 1 MERTAGKELALAPLDQWGEETEDGAVYSVLRQRSPAEQSGQAPSIANTFLH 60
Qy 61 YRTSKVRVLAARLERLVLGDEQDQSPFAFLATYRTFTVPTACLLGFLLLPMPPP 120
Db 61 YRTSKVRVLAARLERLVLGDEQDQSPFAFLATYRTFTVPTACLLGFLLLPMPPP 120
Qy 121 PPPGVEIKKTAVQDLTFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLGSVRTFLGWAAP 180
Db 121 PPPGVEIKKTAVQDLTFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLGSVRTFLGWAAP 180
Qy 181 GSAAQAKAEKLLDEFLFEAEAREQEPPQVMTGPRVAQTSDDPSSEACAEBEGLMPOG 240
Db 181 GSAAQAKAEKLLDEFLFEAEAREQEPPQVMTGPRVAQTSDDPSSEACAEBEGLMPOG 240
Qy 241 POLLDPSVDEVAEQTLIDLELFSKVRLYECLGSVMSQDRDPGAAGASPTVATVAQFNT 300
Db 241 POLLDPSVDEVAEQTLIDLELFSKVRLYECLGSVMSQDRDPGAAGASPTVATVAQFNT 300
Qy 301 VTGCVLGSVLGAPGLAAPQRAQRLKWIARQACRELRFSSRLRALSALQSNPIYRLKR 360
Db 301 VTGCVLGSVLGAPGLAAPQRAQRLKWIARQACRELRFSSRLRALSALQSNPIYRLKR 360
Qy 361 SWGAVSREPLSTFRKLSQIFSDNNHLSGREILFQEEATEGSEEDNTPGSLPKPPGP 420
Db 361 SWGAVSREPLSTFRKLSQIFSDNNHLSGREILFQEEATEGSEEDNTPGSLPKPPGP 420
Qy 421 VPYLGTFTDLVMDLTPALPDMLGDLINFEKRWKEWELIARIQOLRRQCSYTLSPHPPI 480
Db 421 VPYLGTFTDLVMDLTPALPDMLGDLINFEKRWKEWELIARIQOLRRQCSYTLSPHPPI 480
Qy 481 LAALHAQNLTEQSYRLSRVIEPPAASCPSPRIRRRISLTKLSAKLAREKSSSPSGS 540
Db 481 LAALHAQNLTEQSYRLSRVIEPPAASCPSPRIRRRISLTKLSAKLAREKSSSPSGS 540
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QY 541 PGDPSSPTSSVSPGSPSRSDAPAGSPASPGQPGPSTKPLSLDLSPRPFALPLG 600  
Db 541 PGDPSSPTSSVSPGSPSRSDAPAGSPASPGQPGPSTKPLSLDLSPRPFALPLG 600  
QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNVQPMWACD 660  
Db 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNVQPMWACD 660  
QY 661 YQLFQVLPGDRVLLIPDNANFYAMSPVAPRDFMLRRKRGTRNTLSVSPS 710  
Db 661 YQLFQVLPGDRVLLIPDNANFYAMSPVAPRDFMLRRKRGTRNTLSVSPS 710

## RESULT 5

US-10-474-291-9  
; Sequence 9, Application US/10474291  
; Publication No. US20040132043A1  
; GENERAL INFORMATION:  
; APPLICANT: AZIMZAI, Yalda; AU-YOUNG, Janice K.  
; APPLICANT: BATRA, Saijeet; BAUGHN, Mariah R.  
; APPLICANT: BECHA, Shanya D.; BOROWSKY, Mark L.  
; APPLICANT: BURFORD, Neil; DING, Li  
; APPLICANT: ELLIOTT, Vicki S.; EMERLING, Brooke M.  
; APPLICANT: GANDHI, Aneena R.; GIETZEN, Kimberly J.  
; APPLICANT: GRIFFIN, Jennifer A.; HAFALIA, April J.A.  
; APPLICANT: HONCHELL, Cynthia D.; LAL, Preeti G.  
; APPLICANT: LEE, Soo Yeun; LU, Dzung Aina M.  
; APPLICANT: ARVIZU, Chandra S.; RAMKUMAR, Jayalaxmi  
; APPLICANT: REDDY, Roopa M.; SANJANWALA, Madhusudan M.  
; APPLICANT: TANG, Y. Tom; CHAWLA, Narinder K.  
; APPLICANT: WANG, Yu-Mei E.; WARREN, Bridget A.  
; APPLICANT: XU, Yuming; YANG, Junming  
; APPLICANT: YAO, Monique G.; YUE, Henry  
; APPLICANT: ZEBARUJADIAN, Yeganeh  
; TITLE OF INVENTION: PROTEINS ASSOCIATED WITH CELL GROWTH, DIFFERENTIATION, AND DEATH  
; FILE REFERENCE: PI-0417 USN  
; CURRENT APPLICATION NUMBER: US/10/474,291  
; PRIOR FILING DATE: 2003-10-06  
; PRIOR APPLICATION NUMBER: PCT/US02/11152  
; PRIOR FILING DATE: 2002-04-05  
; PRIOR APPLICATION NUMBER: US 60/349,705  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: US 60/295,263  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: US 60/295,340  
; PRIOR FILING DATE: 2001-06-01  
; PRIOR APPLICATION NUMBER: US 60/293,727  
; PRIOR FILING DATE: 2001-05-25  
; PRIOR APPLICATION NUMBER: US 60/291,846  
; PRIOR FILING DATE: 2001-05-18  
; PRIOR APPLICATION NUMBER: US 60/291,662  
; PRIOR FILING DATE: 2001-05-16  
; PRIOR APPLICATION NUMBER: US 60/287,228  
; PRIOR FILING DATE: 2001-04-27  
; PRIOR APPLICATION NUMBER: US 60/286,820  
; PRIOR FILING DATE: 2001-04-26  
; PRIOR APPLICATION NUMBER: US 60/283,294  
; PRIOR FILING DATE: 2001-04-11  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PERL Program  
; SEQ ID NO 9  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc feature  
; OTHER INFORMATION: Incyte ID No: 6937367CD1  
US-10-474-291-9

Query Match 85.8%; Score 609; DB 4; Length 710;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MERTAGKELALAPLDWGEETEDGAVYVSLRQRORRSPAGSGGQAPSPPIANTFLH 60  
Db 1 MERTAGKELALAPLDWGEETEDGAVYVSLRQRORRSPAGSGGQAPSPPIANTFLH 60  
QY 61 YRTSKVRVLAARLERLVGELVFGDREQDPSFMPAFIATYRTFVPTACLLGFLLPMPPPP 120  
Db 61 YRTSKVRVLAARLERLVGELVFGDREQDPSFMPAFIATYRTFVPTACLLGFLLPMPPPP 120  
QY 121 PPGVEIKKTAVQDLSFNKNLRAVSVGLSWLQDHPQDPRDHPVHSDGLSVRTFLGWAAP 180  
Db 121 PPGVEIKKTAVQDLSFNKNLRAVSVGLSWLQDHPQDPRDHPVHSDGLSVRTFLGWAAP 180  
QY 181 GSAEAKAEKLLDFLEAEEREOEPPOVVTGPPRVAQTSDDPSSEACAEEEGLMPOG 240  
Db 181 GSAEAKAEKLLDFLEAEEREOEPPOVVTGPPRVAQTSDDPSSEACAEEEGLMPOG 240  
QY 241 POLLDFSVDEVAEQTLTLDLELFSKVLRYECLGVSVMQDRDPAAGASPTVRATVAQNT 300  
Db 241 POLLDFSVDEVAEQTLTLDLELFSKVLRYECLGVSVMQDRDPAAGASPTVRATVAQNT 300  
QY 301 VTCGVLSVGLGAPGLAAPQRAQRLKWIQAQRCRELNFSSRLAISALQSNIPIYRLKR 360  
Db 301 VTCGVLSVGLGAPGLAAPQRAQRLKWIQAQRCRELNFSSRLAISALQSNIPIYRLKR 360  
QY 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEAETEGSOEDNTGSLPSKPPPGP 420  
Db 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEAETEGSOEDNTGSLPSKPPPGP 420  
QY 421 VPYLGTLTDLVMDLTALPDMLEGLINFEKRWKWEILARIQOLQRRCSYTLSPHPPI 480  
Db 421 VPYLGTLTDLVMDLTALPDMLEGLINFEKRWKWEILARIQOLQRRCSYTLSPHPPI 480  
QY 481 LAALHAQNQLTEQSVRLSRVIEPPAASCPSPIRRIRISLTSLKLSAKLAREKSSSPSGS 540  
Db 481 LAALHAQNQLTEQSVRLSRVIEPPAASCPSPIRRIRISLTSLKLSAKLAREKSSSPSGS 540  
QY 541 PGDPSSPTSSVSPGSPSRSDAPAGSPASPGQPGPSTKPLSLDLSPRPFALPLG 600  
Db 541 PGDPSSPTSSVSPGSPSRSDAPAGSPASPGQPGPSTKPLSLDLSPRPFALPLG 600  
QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNVQPMWACD 660  
Db 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNVQPMWACD 660  
QY 661 YQLFQVLPGDRVLLIPDNANFYAMSPVAPRDFMLRRKRGTRNTLSVSPS 710  
Db 661 YQLFQVLPGDRVLLIPDNANFYAMSPVAPRDFMLRRKRGTRNTLSVSPS 710

## RESULT 6

US-10-894-680A-3  
; Sequence 3, Application US/10894680A  
; Publication No. US20050176021A1  
; GENERAL INFORMATION:  
; APPLICANT: GU, Yizhong  
; APPLICANT: NGUYEN, Cung-Tuong  
; TITLE OF INVENTION: HUMAN RALGDS-LIKE PROTEIN 3  
; FILE REFERENCE: PB0176  
; CURRENT APPLICATION NUMBER: US/10/894,680A  
; CURRENT FILING DATE: 2004-07-19  
; PRIOR APPLICATION NUMBER: 10/060,990  
; PRIOR FILING DATE: 2002-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30

; PRIOR APPLICATION NUMBER: PCT/US01/00668  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670  
 ; PRIOR FILING DATE: 2001-01-30  
 ; PRIOR APPLICATION NUMBER: US 09/864,761  
 ; PRIOR FILING DATE: 2001-05-23  
 ; Remaining Prior Application data removed - See File Wrapper or PALM.  
 ; NUMBER OF SEQ ID NOS: 68  
 ; SOFTWARE: Acomica Sequence Listing Engine  
 ; SEQ ID NO 3  
 ; LENGTH: 710  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-894-680A-3

Query Match 85.8%; Score 609; DB 5; Length 710;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 1   | MERTAGKELALAPLQDWGEETEDGAVYSVLSRRQRESPAEGGSGQAPSPANTFLH     | 60  |
| Db | 1   | MERTAGKELALAPLQDWGEETEDGAVYSVLSRRQRESPAEGGSGQAPSPANTFLH     | 60  |
| Qy | 61  | YRTSKVRVLRARLERLVGELVFGDREODPSFMPAFLATYRTFTACLLGFLLPMPPPP   | 120 |
| Db | 61  | YRTSKVRVLRARLERLVGELVFGDREODPSFMPAFLATYRTFTACLLGFLLPMPPPP   | 120 |
| Qy | 121 | PPPGVEIKTAVQDLSFNKNLRVAVSVLGSWLQDHPQDFRDHPVHSDLGSVRTFLGWAAP | 180 |
| Db | 121 | PPPGVEIKTAVQDLSFNKNLRVAVSVLGSWLQDHPQDFRDHPVHSDLGSVRTFLGWAAP | 180 |
| Qy | 181 | GSAEAKAEKLLDFLEAEAREOEPEEPQVMTGTPRVAQTSDDPDSSEACAEEEGLMPQG  | 240 |
| Db | 181 | GSAEAKAEKLLDFLEAEAREOEPEEPQVMTGTPRVAQTSDDPDSSEACAEEEGLMPQG  | 240 |
| Qy | 241 | PQLDFFSDEVAEQLTLIDLFSKVRLYECLGWSVQSDRPGAGASPTVRATVAQFNT     | 300 |
| Db | 241 | PQLDFFSDEVAEQLTLIDLFSKVRLYECLGWSVQSDRPGAGASPTVRATVAQFNT     | 300 |
| Qy | 301 | VTGCVLGSVLGAPGLAAPQRAQLEKWIRIAQRCRELNFSSLRALISALQSNPIYRLKR  | 360 |
| Db | 301 | VTGCVLGSVLGAPGLAAPQRAQLEKWIRIAQRCRELNFSSLRALISALQSNPIYRLKR  | 360 |
| Qy | 361 | SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEEATEGSEEDNTPGSLPSKPPGP  | 420 |
| Db | 361 | SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEEATEGSEEDNTPGSLPSKPPGP  | 420 |
| Qy | 421 | VPYLGTFITDLVMDLTALPDMLEGLINFEKRRKEWEILARIQOLQRCQSYTLSPHPPI  | 480 |
| Db | 421 | VPYLGTFITDLVMDLTALPDMLEGLINFEKRRKEWEILARIQOLQRCQSYTLSPHPPI  | 480 |
| Qy | 481 | LAALHAQNOLTEQSYRLSRVIEPPAASCPSPRIRRRISITKRLSAKLAREKSSSPGSG  | 540 |
| Db | 481 | LAALHAQNOLTEQSYRLSRVIEPPAASCPSPRIRRRISITKRLSAKLAREKSSSPGSG  | 540 |
| Qy | 541 | PGDSSPTSSVSGSPSSPSRSDAPAGSPASPGQPGPSTKPLPLSLDLPSPRFPALPLG   | 600 |
| Db | 541 | PGDSSPTSSVSGSPSSPSRSDAPAGSPASPGQPGPSTKPLPLSLDLPSPRFPALPLG   | 600 |
| Qy | 601 | SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILITSDQKAPSVRRALQKHNVPQWACD   | 660 |
| Db | 601 | SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILITSDQKAPSVRRALQKHNVPQWACD   | 660 |
| Qy | 661 | YQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS            | 710 |
| Db | 661 | YQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS            | 710 |

RESULT 7  
 US-09-808-701A-33  
 ; Sequence 33, Application US/09808701A

; Publication No. US20020146757A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Goodrich, Ryle  
 ; APPLICANT: Asundi, Vinod  
 ; APPLICANT: Drmanac, Radoje T.  
 ; TITLE OF INVENTION: No. 6610536el Nucleic Acids and  
 ; FILE REFERENCES: 790CIP2D  
 ; CURRENT APPLICATION NUMBER: US/09/808,701A  
 ; CURRENT FILING DATE: 2002-03-14  
 ; PRIOR APPLICATION NUMBER: 09/649,167 ✓  
 ; PRIOR FILING DATE: 2000-08-23  
 ; PRIOR APPLICATION NUMBER: 09/540,217  
 ; PRIOR FILING DATE: 2000-03-31  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: Pct\_Fl\_genes Version 2.0  
 ; SEQ ID NO 33  
 ; LENGTH: 715  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-808-701A-33

Query Match 68.6%; Score 487; DB 3; Length 715;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |   |     |
|----|-----|---|-----|
| Qy | 224 | DSSEACAEEEGLMPQGLLDPSVDEVAEQTLTIDLFSKVRLYECLGWSVQSDRPG      | 283 |
| Db | 229 | DSSEACAEEEGLMPQGLLDPSVDEVAEQTLTIDLFSKVRLYECLGWSVQSDRPG      | 288 |
| Qy | 284 | AAGASPTVRATVAQFNTVTCVLGSLGAPGLAAPQRAQLEKWIRIAQRCRELNFSSL    | 343 |
| Db | 289 | AAGASPTVRATVAQFNTVTCVLGSLGAPGLAAPQRAQLEKWIRIAQRCRELNFSSL    | 348 |
| Qy | 344 | RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEEATEGSO | 403 |
| Db | 349 | RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEEATEGSO | 408 |
| Qy | 404 | EEENTPGSLPSKPPGPGVPYLGTFITDLVMDLTALPDMLEGLINFEKRRKEWEILARIQ | 463 |
| Db | 409 | EEENTPGSLPSKPPGPGVPYLGTFITDLVMDLTALPDMLEGLINFEKRRKEWEILARIQ | 468 |
| Qy | 464 | QLORRCSYTLSPHPPIALHAQNOLTEQSYRLSRVIEPPAASCPSPRIRRRISITK     | 523 |
| Db | 469 | QLORRCSYTLSPHPPIALHAQNOLTEQSYRLSRVIEPPAASCPSPRIRRRISITK     | 528 |
| Qy | 524 | RLSAKLAREKSSPSGSGPGDPSPSTSSVSGSPSSPSRSDAPAGSPASPGQPGPSTKL   | 583 |
| Db | 529 | RLSAKLAREKSSPSGSGPGDPSPSTSSVSGSPSSPSRSDAPAGSPASPGQPGPSTKL   | 588 |
| Qy | 584 | PLSLDLPSPRFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILITSDQKAPSV | 643 |
| Db | 589 | PLSLDLPSPRFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILITSDQKAPSV | 648 |
| Qy | 644 | VRRALQKHNVPQWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN   | 703 |
| Db | 649 | VRRALQKHNVPQWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN   | 708 |
| Qy | 704 | TLVSVPSS  | 710 |
| Db | 709 | TLVSVPSS  | 715 |

RESULT 8  
 US-10-233-131-33  
 ; Sequence 33, Application US/10233131  
 ; Publication No. US20030096279A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tang, Y. Tom  
 ; APPLICANT: Zhou, Ping  
 ; APPLICANT: Goodrich, Ryle  
 ; APPLICANT: Asundi, Vinod

APPLICANT: Zhao, Qing A.  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Xue, Aidong J.  
APPLICANT: Ren, Feiyan  
APPLICANT: Wang, Dunrui  
APPLICANT: Chen, Rui-hong  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. US20030096279A1el Nucleic Acids and  
TITLE OF INVENTION: Polypeptides  
FILE REFERENCE: 790CIP2D DIVA  
CURRENT APPLICATION NUMBER: US/10/233,131  
CURRENT FILING DATE: 2002-08-29  
PRIOR APPLICATION NUMBER: 09/808,701  
PRIOR FILING DATE: 2001-03-14  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: pt\_FL\_genes Version 2.0  
SEQ ID NO 33  
LENGTH: 715  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-233-131-33

Query Match 68.6%; Score 487; DB 4; Length 715;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 224 DSSACAEEEGLMPQGLDPSVDEVAEQTLIDLEFSKVLRYECLGSVWSQRDPG 283  
Db 229 DSSACAEEEGLMPQGLDPSVDEVAEQTLIDLEFSKVLRYECLGSVWSQRDPG 288  
Qy 284 AAGASPTVRATVAQNTVTCVGLSVLGAAPQRAQRLKIRIAQRCRELNFSS 343  
Db 289 AAGASPTVRATVAQNTVTCVGLSVLGAAPQRAQRLKIRIAQRCRELNFSS 348  
Qy 344 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ 403  
Db 349 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ 408  
Qy 404 EEDNTGSLPKPPGPPVYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWILARIQ 463  
Db 409 EEDNTGSLPKPPGPPVYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWILARIQ 468  
Qy 464 QLORRCQSYTLSPHPPIALAAHAQNLTQEQSYRLSRVIEPPAAACSPSSPRIIRRLSLTK 523  
Db 469 QLORRCQSYTLSPHPPIALAAHAQNLTQEQSYRLSRVIEPPAAACSPSSPRIIRRLSLTK 528  
Qy 524 RLSAKLAREKSSSPGSGDPSSPTSSVSGSPSSPSRSDAPAGSPASPSPGPGPSTKL 583  
Db 529 RLSAKLAREKSSSPGSGDPSSPTSSVSGSPSSPSRSDAPAGSPASPSPGPGPSTKL 588  
Qy 584 PLSLDLPSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTTSQDKAPSV 643  
Db 589 PLSLDLPSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTTSQDKAPSV 648  
Qy 644 VRRALQKHNVQPPWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 703  
Db 649 VRRALQKHNVQPPWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 708  
Qy 704 TLSVSPS 710  
Db 709 TLSVSPS 715

RESULT 9  
US-10-240-145-85  
Sequence 85, Application US/10240145  
Publication No. US20030235883A1  
GENERAL INFORMATION:  
APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 21272-048  
CURRENT APPLICATION NUMBER: US/10/240,145  
CURRENT FILING DATE: 2002-09-27  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/668,680  
PRIOR FILING DATE: 2000-09-22  
PRIOR APPLICATION NUMBER: 09/695,618  
PRIOR FILING DATE: 2000-10-23  
PRIOR APPLICATION NUMBER: 09/728,711  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: NOT YET ASSIGNED  
PRIOR FILING DATE: 2000-03-14  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: Custom  
SEQ ID NO 85  
LENGTH: 715  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-240-145-85

Query Match 68.6%; Score 487; DB 4; Length 715;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 224 DSSACAEEEGLMPQGLDPSVDEVAEQTLIDLEFSKVLRYECLGSVWSQRDPG 283  
Db 229 DSSACAEEEGLMPQGLDPSVDEVAEQTLIDLEFSKVLRYECLGSVWSQRDPG 288  
Qy 284 AAGASPTVRATVAQNTVTCVGLSVLGAAPQRAQRLKIRIAQRCRELNFSS 343  
Db 289 AAGASPTVRATVAQNTVTCVGLSVLGAAPQRAQRLKIRIAQRCRELNFSS 348  
Qy 344 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ 403  
Db 349 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ 408  
Qy 404 EEDNTGSLPKPPGPPVYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWILARIQ 463  
Db 409 EEDNTGSLPKPPGPPVYLGTFITDLVMDLTALPDMLEGLDINFEKRRKEWILARIQ 468  
Qy 464 QLORRCQSYTLSPHPPIALAAHAQNLTQEQSYRLSRVIEPPAAACSPSSPRIIRRLSLTK 523  
Db 469 QLORRCQSYTLSPHPPIALAAHAQNLTQEQSYRLSRVIEPPAAACSPSSPRIIRRLSLTK 528  
Qy 524 RLSAKLAREKSSSPGSGDPSSPTSSVSGSPSSPSRSDAPAGSPASPSPGPGPSTKL 583  
Db 529 RLSAKLAREKSSSPGSGDPSSPTSSVSGSPSSPSRSDAPAGSPASPSPGPGPSTKL 588  
Qy 584 PLSLDLPSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTTSQDKAPSV 643  
Db 589 PLSLDLPSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTTSQDKAPSV 648  
Qy 644 VRRALQKHNVQPPWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 703  
Db 649 VRRALQKHNVQPPWACDYQLFQVLPGRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 708  
Qy 704 TLSVSPS 710  
Db 709 TLSVSPS 715

RESULT 10  
US-10-291-128-85  
Sequence 85, Application US/10291128  
Publication No. US20050202422A1  
GENERAL INFORMATION:  
APPLICANT: Nuvelo, Inc  
TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
FILE REFERENCE: 790CIP4



APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6610536el Nucleic Acids and  
FILE REFERENCE: 790CIP2D  
CURRENT APPLICATION NUMBER: US/09/808,701A  
CURRENT FILING DATE: 2002-03-14  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 172  
SOFTWARE: Custom  
SEQ ID NO 85  
LENGTH: 715  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-291-128-85

Query Match 68.6%; Score 487; DB 5; Length 715;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 224 DSSACAEELMPPQGLDQFVDEVAEQLTLDLELFKVKLYECLGVSQDRPQ 283  
Db 229 DSSACAEELMPPQGLDQFVDEVAEQLTLDLELFKVKLYECLGVSQDRPQ 288  
Qy 284 AAGASPTVRATVAQNTVTCVGLGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 343  
Db 289 AAGASPTVRATVAQNTVTCVGLGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 348  
Qy 344 RAILSALQSNPIYRLKRSWGVAREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 403  
Db 349 RAILSALQSNPIYRLKRSWGVAREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 408  
Qy 404 EEDNTPGSLPKPPGPPVYLGTFDLVMDLTDLPMDLEGLDINFEKRRKEWEILARIQ 463  
Db 409 EEDNTPGSLPKPPGPPVYLGTFDLVMDLTDLPMDLEGLDINFEKRRKEWEILARIQ 468  
Qy 464 QLORRCQSYTLSPHPPIALAAHQNLTEQSYRLSRVIEPPAASCPSRRIRRIISLTK 523  
Db 469 QLORRCQSYTLSPHPPIALAAHQNLTEQSYRLSRVIEPPAASCPSRRIRRIISLTK 528  
Qy 524 RLSAKLAREKSSSPGSGDPSSPTSSVSGSPSSPRSDAPAGSPASPQPGPSTKL 583  
Db 529 RLSAKLAREKSSSPGSGDPSSPTSSVSGSPSSPRSDAPAGSPASPQPGPSTKL 588  
Qy 584 PLSLDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 643  
Db 589 PLSLDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 648  
Qy 644 VRRALQKHNVPQWACDYQLFQVLPGRV 672  
Db 649 VRRALQKHNVPQWACDYQLFQVLPGRV 677  
Qy 704 TLSVSPS 710  
Db 709 TLSVSPS 715

RESULT 11  
US-09-808-701A-34  
Sequence 34, Application US/09808701A  
Publication No. US20020146757A1  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Goodrich, Ryle  
APPLICANT: Asundi, Vinod

APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. 6610536el Nucleic Acids and  
FILE REFERENCE: 790CIP2D  
CURRENT APPLICATION NUMBER: US/09/808,701A  
CURRENT FILING DATE: 2002-03-14  
PRIOR APPLICATION NUMBER: 09/649,167  
PRIOR FILING DATE: 2000-08-23  
PRIOR APPLICATION NUMBER: 09/540,217  
PRIOR FILING DATE: 2000-03-31  
NUMBER OF SEQ ID NOS: 34  
SOFTWARE: pt\_FL\_genes Version 2.0  
SEQ ID NO 34  
LENGTH: 699  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-808-701A-34

Query Match 63.2%; Score 449; DB 3; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 224 DSSACAEELMPPQGLDQFVDEVAEQLTLDLELFKVKLYECLGVSQDRPQ 283  
Db 229 DSSACAEELMPPQGLDQFVDEVAEQLTLDLELFKVKLYECLGVSQDRPQ 288  
Qy 284 AAGASPTVRATVAQNTVTCVGLGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 343  
Db 289 AAGASPTVRATVAQNTVTCVGLGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 348  
Qy 344 RAILSALQSNPIYRLKRSWGVAREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 403  
Db 349 RAILSALQSNPIYRLKRSWGVAREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 408  
Qy 404 EEDNTPGSLPKPPGPPVYLGTFDLVMDLTDLPMDLEGLDINFEKRRKEWEILARIQ 463  
Db 409 EEDNTPGSLPKPPGPPVYLGTFDLVMDLTDLPMDLEGLDINFEKRRKEWEILARIQ 468  
Qy 464 QLORRCQSYTLSPHPPIALAAHQNLTEQSYRLSRVIEPPAASCPSRRIRRIISLTK 523  
Db 469 QLORRCQSYTLSPHPPIALAAHQNLTEQSYRLSRVIEPPAASCPSRRIRRIISLTK 528  
Qy 524 RLSAKLAREKSSSPGSGDPSSPTSSVSGSPSSPRSDAPAGSPASPQPGPSTKL 583  
Db 529 RLSAKLAREKSSSPGSGDPSSPTSSVSGSPSSPRSDAPAGSPASPQPGPSTKL 588  
Qy 584 PLSLDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 643  
Db 589 PLSLDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 648  
Qy 644 VRRALQKHNVPQWACDYQLFQVLPGRV 672  
Db 649 VRRALQKHNVPQWACDYQLFQVLPGRV 677

RESULT 12  
US-10-233-131-34  
Sequence 34, Application US/10233131  
Publication No. US20030096279A1  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Zhou, Ping  
APPLICANT: Goodrich, Ryle  
APPLICANT: Asundi, Vinod  
APPLICANT: Zhao, Qing A.  
APPLICANT: Wang, Jian-Rui  
APPLICANT: Xue, Aidong J.  
APPLICANT: Ren, Feiyan  
APPLICANT: Wang, Dunrui  
APPLICANT: Chen, Rui-hong  
APPLICANT: Drmanac, Radoje T.  
TITLE OF INVENTION: No. US20030096279A1el Nucleic Acids and  
TITLE OF INVENTION: Polypeptides

FILE REFERENCE: 790CIP2D DIVA  
; CURRENT APPLICATION NUMBER: US/10/233,131  
; PRIOR FILING DATE: 2002-08-29  
; PRIOR APPLICATION NUMBER: 09/808,701  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: pc\_FU\_genes Version 2.0  
; SEQ ID NO 34  
; LENGTH: 699  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-233-131-34

Query Match 63.2%; Score 449; DB 4; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DSSEACAEEEGLMPQGLDQFVDEVAEQLTLIDLEFSKVRLYECLGVSWSQRDPG 283  
DB 229 DSSEACAEEEGLMPQGLDQFVDEVAEQLTLIDLEFSKVRLYECLGVSWSQRDPG 288  
QY 284 AAGASPTVRATVAQNTVTGCVLGSVGLGAPLAAPQRAQLEKWKIRIAQRCRELNFSS 343  
DB 289 AAGASPTVRATVAQNTVTGCVLGSVGLGAPLAAPQRAQLEKWKIRIAQRCRELNFSS 348  
QY 344 RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 403  
DB 349 RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 408  
QY 404 EEDNTPGSLPKPPGPPVYLTFTDLVMDLTALPDMLEGLINFEKRRKEWILARIQ 463  
DB 409 EEDNTPGSLPKPPGPPVYLTFTDLVMDLTALPDMLEGLINFEKRRKEWILARIQ 468  
QY 464 QLQRCQSYTLSPHPPIALAAHAQNOLTEQSYRLSRVIEPPAACSPSSPRIIRISLTK 523  
DB 469 QLQRCQSYTLSPHPPIALAAHAQNOLTEQSYRLSRVIEPPAACSPSSPRIIRISLTK 528  
QY 524 RLSAKLAREKSSPSGSPGDPSSPTSSVSPGSPSSPRSDAPAGSPAPSPGPGPSTKL 583  
DB 529 RLSAKLAREKSSPSGSPGDPSSPTSSVSPGSPSSPRSDAPAGSPAPSPGPGPSTKL 588  
QY 584 PLSLDLPSPRPFPALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 643  
DB 589 PLSLDLPSPRPFPALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 648

RESULT 13  
US-10-240-145-86  
; Sequence 86, Application US/10240145  
; Publication No. US20030235883A1  
; GENERAL INFORMATION:  
; APPLICANT: Hyseq, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 21272-048  
; CURRENT APPLICATION NUMBER: US/10/240,145  
; PRIOR FILING DATE: 2002-09-27  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: 09/668,680  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/695,618  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 09/728,711

PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: NOT YET ASSIGNED  
; PRIOR FILING DATE: 2000-03-14  
; NUMBER OF SEQ ID NOS: 172  
; SOFTWARE: Custom  
; SEQ ID NO 86  
; LENGTH: 699  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-240-145-86

Query Match 63.2%; Score 449; DB 4; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DSSEACAEEEGLMPQGLDQFVDEVAEQLTLIDLEFSKVRLYECLGVSWSQRDPG 283  
DB 229 DSSEACAEEEGLMPQGLDQFVDEVAEQLTLIDLEFSKVRLYECLGVSWSQRDPG 288  
QY 284 AAGASPTVRATVAQNTVTGCVLGSVGLGAPLAAPQRAQLEKWKIRIAQRCRELNFSS 343  
DB 289 AAGASPTVRATVAQNTVTGCVLGSVGLGAPLAAPQRAQLEKWKIRIAQRCRELNFSS 348  
QY 344 RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 403  
DB 349 RAILSALQSNPIYRLKRWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 408  
QY 404 EEDNTPGSLPKPPGPPVYLTFTDLVMDLTALPDMLEGLINFEKRRKEWILARIQ 463  
DB 409 EEDNTPGSLPKPPGPPVYLTFTDLVMDLTALPDMLEGLINFEKRRKEWILARIQ 468  
QY 464 QLQRCQSYTLSPHPPIALAAHAQNOLTEQSYRLSRVIEPPAACSPSSPRIIRISLTK 523  
DB 469 QLQRCQSYTLSPHPPIALAAHAQNOLTEQSYRLSRVIEPPAACSPSSPRIIRISLTK 528  
QY 524 RLSAKLAREKSSPSGSPGDPSSPTSSVSPGSPSSPRSDAPAGSPAPSPGPGPSTKL 583  
DB 529 RLSAKLAREKSSPSGSPGDPSSPTSSVSPGSPSSPRSDAPAGSPAPSPGPGPSTKL 588  
QY 584 PLSLDLPSPRPFPALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 643  
DB 589 PLSLDLPSPRPFPALPLGSPRIPLPAQOSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 648

RESULT 14  
US-10-291-128-86  
; Sequence 86, Application US/10291128  
; Publication No. US20050202422A1  
; GENERAL INFORMATION:  
; APPLICANT: Nuvelo, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP4  
; CURRENT APPLICATION NUMBER: US/10/291,128  
; CURRENT FILING DATE: 2002-11-08  
; PRIOR APPLICATION NUMBER: PCT/US01/10484  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR APPLICATION NUMBER: 09/668,680  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 09/695,618  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 09/728,711  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: 09/808,701  
; PRIOR FILING DATE: 2001-03-14  
; NUMBER OF SEQ ID NOS: 172



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; SOFTWARE: Custom
; SEQ ID NO 86
; LENGTH: 699
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-128-86

Query Match      63.2%; Score 449; DB 5; Length 699;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 DSSACAEELMPQGLDFFSDEVAEOLTLIDLELFSKRLVECLGWSVMSQDRPG 283
Db 229 DSSACAEELMPQGLDFFSDEVAEOLTLIDLELFSKRLVECLGWSVMSQDRPG 288
Qy 284 AAGASPTVRATVAQNTVTGCVLGVGAPGLAAPQRAQLEKWIIRIAQRCRELNFSS 343
Db 289 AAGASPTVRATVAQNTVTGCVLGVGAPGLAAPQRAQLEKWIIRIAQRCRELNFSS 348
Qy 344 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 403
Db 349 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQ 408
Qy 404 EEDNTPGSLPKPPPPVPYLGTFITDLVMDLTDALPDMLEGLDINFEKRRKEWEILARIQ 463
Db 409 EEDNTPGSLPKPPPPVPYLGTFITDLVMDLTDALPDMLEGLDINFEKRRKEWEILARIQ 468
Qy 464 QLQRCSQYTLSPHPPIILAAHQAQNLTEEQSYRLSRVIEPPAASCPSPIRRIRISLTK 523
Db 469 QLQRCSQYTLSPHPPIILAAHQAQNLTEEQSYRLSRVIEPPAASCPSPIRRIRISLTK 528
Qy 524 RLSAKLAREKSSSPGSDPTSSVSGSPSSPRSRDAPAGSPASPAGSPGQPTKL 583
Db 529 RLSAKLAREKSSSPGSDPTSSVSGSPSSPRSRDAPAGSPASPAGSPGQPTKL 588
Qy 584 PLSLDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 643
Db 589 PLSLDLPSRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 648
Qy 644 VRRALQKHNPQWACDYQLFQVLPGRV 672
Db 649 VRRALQKHNPQWACDYQLFQVLPGRV 677
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RESULT 15
US-10-094-749-2959
; Sequence 2959, Application US/10094749
; Publication No. US20030219741A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOKUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: NOVEL FULL-LENGTH cDNA
; FILE REFERENCE: 084335/0160
; CURRENT APPLICATION NUMBER: US/10/094,749
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/350,435
; PRIOR FILING DATE: 2002-01-24
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; PRIOR APPLICATION NUMBER: JP 2001-328381
; PRIOR FILING DATE: 2001-09-14
; NUMBER OF SEQ ID NOS: 3381
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2959
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-094-749-2959
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Query Match      61.3%; Score 435; DB 4; Length 464;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 237 MPOGPQLDFFSDEVAEOLTLIDLELFSKRLVECLGWSVMSQDRPGAAGASPTVRATVA 296
Db 1 MPOGPQLDFFSDEVAEOLTLIDLELFSKRLVECLGWSVMSQDRPGAAGASPTVRATVA 60
Qy 297 QFNTVTGCVLGVGAPGLAAPQRAQLEKWIIRIAQRCRELNFSSRLAISALQSNPIY 356
Db 61 QFNTVTGCVLGVGAPGLAAPQRAQLEKWIIRIAQRCRELNFSSRLAISALQSNPIY 120
Qy 357 RLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQEDNTPGSLPKP 416
Db 121 RLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSQEDNTPGSLPKP 180
Qy 417 PGPVPVYLGTFITDLVMDLTDALPDMLEGLDINFEKRRKEWEILARIQOLQRCSQYTLSP 476
Db 181 PGPVPVYLGTFITDLVMDLTDALPDMLEGLDINFEKRRKEWEILARIQOLQRCSQYTLSP 240
Qy 477 HPPIILAAHQAQNLTEEQSYRLSRVIEPPAASCPSPIRRIRISLTKRLSAKLAREKSSS 536
Db 241 HPPIILAAHQAQNLTEEQSYRLSRVIEPPAASCPSPIRRIRISLTKRLSAKLAREKSSS 300
Qy 537 PGSGPDPSPTSSVSGSPSSPRSRDAPAGSPASPAGSPGQPTKLPLSLDLPSPRPPFA 596
Db 301 PGSGPDPSPTSSVSGSPSSPRSRDAPAGSPASPAGSPGQPTKLPLSLDLPSPRPPFA 360
Qy 597 LPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNPQ 656
Db 361 LPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRRALQKHNPQ 420
Qy 657 WACDYQLFQVLPGRD 671
Db 421 WACDYQLFQVLPGRD 435
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Search completed: June 12, 2006, 12:20:19
Job time : 183 secs
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GenCore version 5.1.9  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: June 12, 2006, 11:55:55 ; Search time 202 Seconds  
(without alignments)  
1607.048 Million cell updates/sec

Title: US-10-694-438-2

Perfect score: 710

Sequence: 1 MERTAGKELALPLQDWGEE.....RDFMLRRKGRNTLSVSPS 710

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2589679 seqs, 457216429 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2589342

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

A Geneseq\_8.\*

- 1: geneseqp1980s.\*
- 2: geneseqp1990s.\*
- 3: geneseqp2000s.\*
- 4: geneseqp2001s.\*
- 5: geneseqp2002s.\*
- 6: geneseqp2003as.\*
- 7: geneseqp2003bs.\*
- 8: geneseqp2004s.\*
- 9: geneseqp2005s.\*
- 10: geneseqp2006s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description        |
|------------|-------|-------------|--------|-------|--------------------|
| 1          | 710   | 100.0       | 710    | 6     | ABP57918 Human Ras |
| 2          | 609   | 85.8        | 710    | 5     | AAO15655 Human Ral |
| 3          | 609   | 85.8        | 710    | 6     | ABP58338 Human cel |
| 4          | 487   | 68.6        | 715    | 6     | AAU68555 Human nov |
| 5          | 487   | 68.6        | 715    | 9     | AED08221 Mouse Ral |
| 6          | 449   | 63.2        | 699    | 4     | AAU68556 Human nov |
| 7          | 449   | 63.2        | 699    | 9     | AED08222 Mouse Ral |
| 8          | 435   | 61.3        | 464    | 6     | ADA55391 Human pro |
| 9          | 384   | 54.1        | 562    | 6     | ABR41327 Human DIT |
| 10         | 381   | 53.7        | 708    | 6     | ABO15021 Human NOV |
| 11         | 207   | 29.2        | 208    | 7     | ADM05268 Human pro |
| 12         | 207   | 29.2        | 208    | 9     | AEC88198 Human CDN |
| 13         | 48    | 6.8         | 70     | 4     | AAU20233 Peptide # |
| 14         | 48    | 6.8         | 70     | 4     | ABB40566 Peptide # |
| 15         | 48    | 6.8         | 70     | 4     | AAU34328 Peptide # |
| 16         | 48    | 6.8         | 70     | 4     | ABB24860 Protein # |
| 17         | 48    | 6.8         | 70     | 4     | AAU74214 Human bon |
| 18         | 48    | 6.8         | 70     | 4     | AAU61424 Human bra |
| 19         | 48    | 6.8         | 70     | 4     | ABG56017 Human liv |
| 20         | 48    | 6.8         | 70     | 5     | ABG44171 Human pep |
| 21         | 26    | 3.7         | 26     | 10    | AEE38096 Human ser |
| 22         | 20    | 2.8         | 20     | 5     | AAO15656 Human Ral |
| 23         | 17    | 2.4         | 677    | 4     | AAU21657 Novel hum |

#### ALIGNMENTS

##### RESULT 1

ABP57918  
ID ABP57918 standard; protein; 710 AA.

XX  
AC ABP57918;

XX  
DT 17-FEB-2003 (first entry)

XX  
DE Human Ras-like protein.

XX  
XX Human; Ras-like protein; antiinflammatory; cytostatic; gene therapy;

XX  
KW Human; inflammation; cancer.

XX  
OS Homo sapiens.

XX  
FN WO200283915-A2.

XX  
XX 24-OCT-2002.

XX  
PF 10-APR-2002; 2002WO-USO11111.

XX  
PR 10-APR-2001; 2001US-0282460P.

XX  
PR 09-APR-2002; 2002US-00118328.

XX  
PA (PEKE ) PE CORP NY.

XX  
PI Yan C, Ketchum KA, Beasley EM;

XX  
DR WPI; 2003-093028/08.

XX  
DR N-PSDB; ABV99729, ABV99730.

XX  
FT New Ras-like protein polypeptides and polynucleotides are useful in diagnosing, treating or preventing inflammation and disorders associated with cell proliferation and apoptosis, particularly cancer.

XX  
PS Claim 1; Fig 2; 98pp; English.

XX  
CC The invention relates to a novel human Ras-like protein. The protein of the invention has antiinflammatory and cytostatic activity. The polynucleotide encoding the Ras-like protein may have a use in gene therapy. The Ras-like protein polypeptides and polynucleotides are useful in diagnosing, treating or preventing inflammation and disorders associated with cell proliferation and apoptosis, particularly cancer.

XX  
SQ Sequence 710 AA;

Adc46298 Human neo  
Aay31246 Murine ral  
Aab23176 Human Ral  
Aam80136 Human pro  
Ade56968 Rat Prote  
Add45418 Rat Prote  
Ade56972 Rat Prote  
Abu08501 Human GTP  
Ade09315 Human pro  
Ade45420 Human pro  
Ade56970 Human pro  
Ade56974 Human pro  
Aam79152 Human pro  
Aam21577 Novel hum  
Aam89022 Human imm  
Adc46218 Human neo  
Aee04919 Cancer-as  
Aee04908 Cancer-as  
Aaw00811 Ras p21 i  
Aay31244 Human RGL  
Add18992 Human dis  
Adr14347 Human NF-

Query Match 100.0%; Score 710; DB 6; Length 710;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 710; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MERTAGKELALAPLDWGEETEDGAVYSVLSRRQRRSPAEFGGSGQAPSPFIANTFLH 60

QY 61 YRTSKVRLRAARLERLVGELVFGDREQDPSFMPAFATYRTFVPTACLLGFLLPMPPP 120  
DB 61 YRTSKVRLRAARLERLVGELVFGDREQDPSFMPAFATYRTFVPTACLLGFLLPMPPP 120

QY 121 PPPGVEIKKTAVQDLSPFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLGSVRTFLGWAAP 180  
DB 121 PPPGVEIKKTAVQDLSPFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLGSVRTFLGWAAP 180

QY 181 GSAAQKAEKLLDFLEEAEREQEPEPPQVWTGPPRVAQTSDFDSSEACAEEEGLMPQG 240  
DB 181 GSAAQKAEKLLDFLEEAEREQEPEPPQVWTGPPRVAQTSDFDSSEACAEEEGLMPQG 240

QY 241 POLLDPSVDEVAEQLTLIDLELFSKVLYECLGSVWSQDRDPAAGASPTVATVAQNT 300  
DB 241 POLLDPSVDEVAEQLTLIDLELFSKVLYECLGSVWSQDRDPAAGASPTVATVAQNT 300

QY 301 VTGCVLSVLGAPGLAAPQRAQRLKWRIRIAQRCRELNFSSRLAILSALQSNPIYRLKR 360  
DB 301 VTGCVLSVLGAPGLAAPQRAQRLKWRIRIAQRCRELNFSSRLAILSALQSNPIYRLKR 360

QY 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSGQEDNTPGSLPKPPGP 420  
DB 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSGQEDNTPGSLPKPPGP 420

QY 421 VPIYLTFTDLVMDLTALPDMLGDLINFEKRRKEWEILARIQOLQRCQSYTILSPHPI 480  
DB 421 VPIYLTFTDLVMDLTALPDMLGDLINFEKRRKEWEILARIQOLQRCQSYTILSPHPI 480

QY 481 LAALHAQNLTEBQSVRLSRVIEPPAASCSPRRIRRRISLTKRLSAKLAREKSSPSGS 540  
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QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVVRALQKHNVQPWACD 660  
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QY 661 YQLFOVLPQDRVLLIPDNNANVFYAMSPVAPRDFMLRRKEGTRNTLSVSPS 710  
DB 661 YQLFOVLPQDRVLLIPDNNANVFYAMSPVAPRDFMLRRKEGTRNTLSVSPS 710

RESULT 2

AAO15655  
ID AAO15655 standard; protein; 710 AA.

AC AAO15655;  
XX AAO15655;

DT 31-OCT-2002 (first entry)

DE Human RalGDS-like protein 3 (RGL3).

XX Human; RalGDS-like protein 3; RGL3 associated disorder;  
KW guanine nucleotide exchange factor; RGL3; gene therapy.

XX Homo sapiens.

XX EP1229132-A2.

XX 07-AUG-2002.

XX

PF 25-JAN-2002; 2002EP-00001159.  
XX 30-JAN-2001; 2001WO-US0000563.  
PR 30-JAN-2001; 2001WO-US0000564.  
PR 30-JAN-2001; 2001WO-US0000565.  
PR 30-JAN-2001; 2001WO-US0000566.  
PR 30-JAN-2001; 2001WO-US0000567.  
PR 30-JAN-2001; 2001WO-US0000568.  
PR 30-JAN-2001; 2001WO-US0000569.  
PR 30-JAN-2001; 2001WO-US0000570.  
PR 23-MAY-2001; 2001US-00864761.  
PR 28-SEP-2001; 2001US-0326105P.  
XX (AEOM-) AEOMICA INC.  
XX Gu Y, Nguyen C;  
PI WPI; 2002-620726/67.  
XX N-PSDB; AAL44435.  
XX Novel RalGDS-like protein 3, a guanine nucleotide exchange factor for  
PT small GTPase Ral and downstream effector for both Rlt and Ras and nucleic  
PT acid encoding it for diagnosing, treating disorders associated with RGL3.  
XX Claim 13; Fig 3; 60pp; English.  
XX The invention comprises the amino acid and coding sequence of the human  
CC RalGDS-like protein 3 (RGL3). RGL3 is a guanine nucleotide exchange  
CC factor for the small GTPase Ral and a downstream effector for both Rlt  
CC and Ras. The RGL3 DNA and protein sequences of the invention are useful  
CC for the diagnosis and treatment/prevention (e.g. gene therapy) of a  
CC disorder associated with decreased or increased expression or activity of  
CC human RGL3. The present amino acid sequence represents the human RGL3  
CC protein  
XX Sequence 710 AA;

Query Match 85.8%; Score 609; DB 5; Length 710;  
Best Local Similarity 99.9%; Pred. No. 0;  
Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 YRTSKVRLRAARLERLVGELVFGDREQDPSFMPAFATYRTFVPTACLLGFLLPMPPP 120  
DB 61 YRTSKVRLRAARLERLVGELVFGDREQDPSFMPAFATYRTFVPTACLLGFLLPMPPP 120

QY 121 PPPGVEIKKTAVQDLSPFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLGSVRTFLGWAAP 180  
DB 121 PPPGVEIKKTAVQDLSPFNKNLRAVSVLGSWLQDHPQDFRDHPVHSDLGSVRTFLGWAAP 180

QY 181 GSAAQKAEKLLDFLEEAEREQEPEPPQVWTGPPRVAQTSDFDSSEACAEEEGLMPQG 240  
DB 181 GSAAQKAEKLLDFLEEAEREQEPEPPQVWTGPPRVAQTSDFDSSEACAEEEGLMPQG 240

QY 241 POLLDPSVDEVAEQLTLIDLELFSKVLYECLGSVWSQDRDPAAGASPTVATVAQNT 300  
DB 241 POLLDPSVDEVAEQLTLIDLELFSKVLYECLGSVWSQDRDPAAGASPTVATVAQNT 300

QY 301 VTGCVLSVLGAPGLAAPQRAQRLKWRIRIAQRCRELNFSSRLAILSALQSNPIYRLKR 360  
DB 301 VTGCVLSVLGAPGLAAPQRAQRLKWRIRIAQRCRELNFSSRLAILSALQSNPIYRLKR 360

QY 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSGQEDNTPGSLPKPPGP 420  
DB 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSGQEDNTPGSLPKPPGP 420

QY 421 VPIYLTFTDLVMDLTALPDMLGDLINFEKRRKEWEILARIQOLQRCQSYTILSPHPI 480  
DB 421 VPIYLTFTDLVMDLTALPDMLGDLINFEKRRKEWEILARIQOLQRCQSYTILSPHPI 480

QY 481 LAALHAQNQLTEQSYRLSRVIEPPAASCPSSPRIIRRIISLTAKLAKLAREKSSSPSGS 540  
 Db |||||  
 QY 481 LAALHAQNQLTEQSYRLSRVIEPPAASCPSSPRIIRRIISLTAKLAKLAREKSSSPSGS 540  
 Db |||||  
 QY 541 PGDPSSPTSSVSGSPSSPRSDAPAGSPGPGQSTKPLSLDLPSRPFALPLG 600  
 Db |||||  
 QY 541 PGDPSSPTSSVSGSPSSPRSDAPAGSPGPGQSTKPLSLDLPSRPFALPLG 600  
 Db |||||  
 QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSIILLTSQDKAPSVVRALOKHNVPQWACD 660  
 Db |||||  
 QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSIILLTSQDKAPSVVRALOKHNVPQWACD 660  
 Db |||||  
 QY 661 YQLFQVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710  
 Db |||||  
 QY 661 YQLFQVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710  
 Db |||||

RESULT 3  
 ABP58338  
 ID ABP58338 standard; protein; 710 AA.  
 AC ABP58338;  
 XX  
 XX  
 DT 07-APR-2003 (first entry)  
 XX  
 XX Human cell growth, differentiation and death protein CGDD-9.  
 XX  
 XX CGDD-9; cell growth; cell differentiation; cell death; human; cytostatic;  
 KW antiarteriosclerotic; hepatotropic; antiinflammatory; antipsoriatic;  
 KW antianaemic; ophthalmologic; auditory; anticonvulsant;  
 KW cerebroprotective; neurotropic; neuroprotective; antiparkinsonian;  
 KW neuroleptic; tranquillizer; immunosuppressive; anti-HIV; anti-allergic;  
 KW antiasthmatic; antithyroid; antidiabetic; dermatological; nephrotropic;  
 KW antirheumatic; antiarthritic; antitumor; antileukemic; antineoplastic;  
 KW antibacterial; fungicide; antiparasitic; protozoacide; antihelminthic;  
 KW antifertility; gynaecological; guanine nucleotide dissociation factor;  
 KW gene therapy.  
 XX  
 XX Homo sapiens.  
 XX  
 PN WO200297032-A2.  
 XX  
 XX 05-DEC-2002.  
 XX  
 XX 05-APR-2002; 2002WO-US011152.  
 XX  
 PR 06-APR-2001; 2001US-0282110P.  
 PR 11-APR-2001; 2001US-0283294P.  
 PR 26-APR-2001; 2001US-0286820P.  
 PR 27-APR-2001; 2001US-0287228P.  
 PR 16-MAY-2001; 2001US-0291662P.  
 PR 18-MAY-2001; 2001US-0291846P.  
 PR 25-MAY-2001; 2001US-0293772P.  
 PR 01-JUN-2001; 2001US-0295263P.  
 PR 01-JUN-2001; 2001US-0295340P.  
 PR 15-JAN-2002; 2002US-0349705P.  
 XX  
 XX (INCY-) INCYTE GENOMICS INC.  
 XX  
 PA Azimzai Y, Au-Young JK, Batra S, Baughn MR, Becha SD;  
 PI Borowsky ML, Burford N, Ding L, Elliott VS, Emerling BM, Gandhi AR;  
 PI Gietzen KJ, Griffin JA, Hafalia AJA, Honchell CD, Lal PG, Lee SY;  
 PI Lu DAM, Arvizu' CS, Ramkumar J, Reddy R, Sanjanwala MM, Tang YF;  
 PI Walia NK, Wang YE, Warren BA, Xu Y, Yang J, Yao MG, Yue H;  
 PI Zebardjian Y;  
 XX  
 XX WPI; 2003-140453/13.  
 DR N-PSDB; AB224697.  
 XX  
 PT Novel human proteins associated with cell growth, differentiation and  
 PT death, useful for treating, diagnosing or preventing cancer,  
 PT developmental, neurological, reproductive or autoimmune/inflammatory  
 PT disorders.

XX  
 PS  
 XX Claim 1; Page 196-197; 238pp; English.  
 CC The present sequence is the protein sequence of human CGDD-9, a novel  
 CC protein associated with cell growth, differentiation and death. The  
 CC sequence is predicted from Incyte clone 6937367CB1, which was isolated  
 CC from a fallopian tube tissue cDNA library. Structural features establish  
 CC the protein as being associated with cell growth, differentiation and  
 CC death, and further evidence suggests it to be a guanine nucleotide  
 CC dissociation factor. The invention is based on novel human CGDD-1 to -21  
 CC proteins (see ABP58330-50), the polynucleotides encoding them (see  
 CC AB224699-709), and to the use of these for the diagnosis, treatment or  
 CC prevention of cell proliferative disorders including cancer,  
 CC developmental disorders, neurological disorders, autoimmune disorders,  
 CC reproductive disorders, and disorders of the placenta, and in the  
 CC assessment of the effects of exogenous compounds on the activity and  
 CC expression of proteins and nucleic acids associated with cell growth,  
 CC differentiation and death  
 XX  
 SQ Sequence 710. AA;  
 Query Match 85.8%; Score 609; DB 6; Length 710;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 709; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MERTAGKELALAPQDWEETEDGAVYSVLRORRORRSPAEPPGSGQAPSPFIANTFLH 60  
 Db |||||  
 QY 1 MERTAGKELALAPQDWEETEDGAVYSVLRORRORRSPAEPPGSGQAPSPFIANTFLH 60  
 Db |||||  
 QY 61 YRTSKVRVLAARLERLVGELVFGDQDPSFMPAFATYRTFTVFTACILGFLLLPMPPP 120  
 Db |||||  
 QY 61 YRTSKVRVLAARLERLVGELVFGDQDPSFMPAFATYRTFTVFTACILGFLLLPMPPP 120  
 Db |||||  
 QY 121 PPPGVEIKKTAQVQLSFNKNLRAVVSGLWQLDHPQFRDHPVHSDLSGVTFLGWAAP 180  
 Db |||||  
 QY 121 PPPGVEIKKTAQVQLSFNKNLRAVVSGLWQLDHPQFRDHPVHSDLSGVTFLGWAAP 180  
 Db |||||  
 QY 181 GSAEAQKAEKLEDFLEAEAREEQEPPQVGTGPRVAQTSDDPDSSEACAEEEGLMPOG 240  
 Db |||||  
 QY 181 GSAEAQKAEKLEDFLEAEAREEQEPPQVGTGPRVAQTSDDPDSSEACAEEEGLMPOG 240  
 Db |||||  
 QY 241 PQLLDFSVDVAEQTLTDLFELSKVRLYECLGVSWSQDRPFGAGASPTVRATVAQNT 300  
 Db |||||  
 QY 241 PQLLDFSVDVAEQTLTDLFELSKVRLYECLGVSWSQDRPFGAGASPTVRATVAQNT 300  
 Db |||||  
 QY 301 VTGCVLGSVLGAPGLAAPQRAQRLKWIIRIAQRCRELNFSSRLAILSALQSNPIYRLKR 360  
 Db |||||  
 QY 301 VTGCVLGSVLGAPGLAAPQRAQRLKWIIRIAQRCRELNFSSRLAILSALQSNPIYRLKR 360  
 Db |||||  
 QY 361 SWGAVSRPLSTFRKLSQIFSDENNHLSSRIILFOEATEGSOEDNTPGSLPSKPPGP 420  
 Db |||||  
 QY 361 SWGAVSRPLSTFRKLSQIFSDENNHLSSRIILFOEATEGSOEDNTPGSLPSKPPGP 420  
 Db |||||  
 QY 421 VPYLGFTLTLVMDLTALPDMLEGLDINFEKRRKEWEILARIQQLQRCQSVTLSPHPPI 480  
 Db |||||  
 QY 421 VPYLGFTLTLVMDLTALPDMLEGLDINFEKRRKEWEILARIQQLQRCQSVTLSPHPPI 480  
 Db |||||  
 QY 481 LAALHAQNQLTEQSYRLSRVIEPPAASCPSSPRIIRRIISLTAKLAKLAREKSSSPSGS 540  
 Db |||||  
 QY 481 LAALHAQNQLTEQSYRLSRVIEPPAASCPSSPRIIRRIISLTAKLAKLAREKSSSPSGS 540  
 Db |||||  
 QY 541 PGDPSSPTSSVSGSPSSPRSDAPAGSPGPGQSTKPLSLDLPSRPFALPLG 600  
 Db |||||  
 QY 541 PGDPSSPTSSVSGSPSSPRSDAPAGSPGPGQSTKPLSLDLPSRPFALPLG 600  
 Db |||||  
 QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSIILLTSQDKAPSVVRALOKHNVPQWACD 660  
 Db |||||  
 QY 601 SPRIPLPAQSSSEARVIRVSDNDHGNLYRSIILLTSQDKAPSVVRALOKHNVPQWACD 660  
 Db |||||  
 QY 661 YQLFQVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710  
 Db |||||  
 QY 661 YQLFQVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRNTLSVSPS 710  
 Db |||||

|          |   |
|----------|---|
| RESULT 5 |   |
| AED08221 |   |
| ID       | AED08221 standard; protein; 715 AA.                                       |
| XX       |   |
| XX       | AED08221;   |
| XX       |   |
| XX       | 17-NOV-2005 (first entry)   |
| DT       |   |
| DE       | Mouse RalGDS-like protein 3 SEQ ID NO: 85.                                |
| XX       |   |
| XX       | Immune stimulation; gene therapy; drug screening; transgenic animal;      |
| XX       | food; inflammation; antiinflammatory; autoimmune disease;                 |
| KW       | immunosuppressive; immune disorder; autonomic nervous system disease;     |
| KW       | cns-gen.; neurological disease; central nervous system disease; leukemia; |
| KW       | cytostatic; hematological disease; neoplasm; RalGDS-like protein 3.       |
| XX       |   |
| XX       | Mus musculus.   |
| OS       |   |
| XX       |   |

PN US2005202422-A1.  
 PD 15-SEP-2005.  
 PF 08-NOV-2002; 2002US-00291128.  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 30-MAR-2001; 2001WO-US010484.  
 XX (TANG/) TANG Y T.  
 PA (LIUC/) LIU C.  
 PA (ASUN/) ASUNDI V.  
 PA (CHEN/) CHEN R.  
 PA (REN/) REN F.  
 PA (WANG/) WANG D.  
 PA (WANG/) WANG J.  
 PA (XUCC/) XU C.  
 PA (XUEA/) XUE A. J.  
 PA (YANG/) YANG Y.  
 PA (ZHAN/) ZHANG J.  
 PA (ZHAO/) ZHAO Q A.  
 PA (ZHOU/) ZHOU P.  
 PA (GOOD/) GOODRICH R W.  
 PA (DRWA/) DRWANAC R T.  
 XX  
 PI Tang YT, Liu C, Asundi V, Chen R, Ren F, Wang D, Wang J, Xu C;  
 PI Xue AJ, Yang Y, Zhang J, Zhao QA, Zhou P, Goodrich RW, Drmanac RT;  
 XX  
 DR WPI; 2005-618089/63.  
 DR N-PSDB; AED08178.  
 XX  
 PT New isolated polynucleotides, useful for treating, preventing, or  
 PT ameliorating, e.g. Alzheimer's disease, Parkinson's disease, Huntington's  
 PT disease, amyotrophic lateral sclerosis, or leukemia.  
 XX  
 PS Claim 20; SEQ ID NO 85; 60pp; English.  
 XX  
 CC The invention relates to polynucleotides and polypeptides capable of  
 CC inducing an immune response. The polynucleotides and proteins are useful  
 CC for treating, preventing or ameliorating a medical condition, e.g.  
 CC Alzheimer's disease, Parkinson's disease, Huntington's disease,  
 CC amyotrophic lateral sclerosis, Shy-Drager syndrome or stroke. The  
 CC proteins can be used for treating leukemia, inflammatory disorders and  
 CC autoimmune disorders, e.g. multiple sclerosis, rheumatoid arthritis,  
 CC diabetes, myasthenia gravis or autoimmune inflammatory eye disease. They  
 CC can also be used as nutritional sources and supplements, e.g. as a carbon  
 CC source, nitrogen source or carbohydrate source. The sequences of the  
 CC invention are also useful in gene therapy, drug screening and in  
 CC production of transgenic animals. The present sequence is the mouse  
 CC RalGDS-like protein 3 of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?docID=20050202422.  
 XX  
 SQ Sequence 715 AA;

Query Match 68.6%; Score 487; DB 9; Length 715;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 224 DSSBACAEELGMPQGGPQLLDVDFVAEQLTDLIDELFSKVLRYECLGSVWQRPRG 283  
 Db 229 DSSBACAEELGMPQGGPQLLDVDFVAEQLTDLIDELFSKVLRYECLGSVWQRPRG 288  
 Qy 284 AAGASPTVRATVAQNTVTGCVLGSVLGAPGLAPQRAQLRKIRIAQRCRELNFSS 343  
 Db 289 AAGASPTVRATVAQNTVTGCVLGSVLGAPGLAPQRAQLRKIRIAQRCRELNFSS 348  
 Qy 344 RAILSALQSNFIYRLKRSWGAVSREPLSTFFKLQIFSDENNHLSSREILFQEBATEGSQ 403  
 Db 349 RAILSALQSNFIYRLKRSWGAVSREPLSTFFKLQIFSDENNHLSSREILFQEBATEGSQ 408  
 Qy 404 EEDNTPGSLPKPPPGPVYLTDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 463

Db 409 EEDNTPGSLPKPPPGPVYLTDLVMDLTALPDMLEGLDINFEKRRKEWEILARIQ 468  
 Qy 464 QLQRRCSYTLSPHPPIALAHQNLTEQSYRLSRVIEPPAAACSPSPRIRRIISLTK 523  
 Db 469 QLQRRCSYTLSPHPPIALAHQNLTEQSYRLSRVIEPPAAACSPSPRIRRIISLTK 528  
 Qy 524 RLSAKLAREKSSSPSGSPGDPSPPTSSVSPGSPSPSRSDAPAGSPASPQGPSTKL 583  
 Db 529 RLSAKLAREKSSSPSGSPGDPSPPTSSVSPGSPSPSRSDAPAGSPASPQGPSTKL 588  
 Qy 584 PLSLDLSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSDQKAPSV 643  
 Db 589 PLSLDLSPRPFPALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSDQKAPSV 648  
 Qy 644 VRRALQKHNVQPPWACDYQLFOVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 703  
 Db 649 VRRALQKHNVQPPWACDYQLFOVLPGDRVLLIPDNANVFYAMSPVAPRDFMLRKEGTRN 708  
 Qy 704 TLSVSPS 710  
 Db 709 TLSVSPS 715

RESULT 6  
 AAU68556  
 ID AAU68556 standard; protein; 699 AA.  
 XX  
 AC AAU68556;  
 XX  
 DT 16-JAN-2002 (first entry)  
 DE Human novel cytokine encoded by cDNA 790CIP2D\_17 #1.  
 KW Human; cytokine; cell proliferation; cell differentiation;  
 KW antiinflammatory; stem cell growth factor; activin; inhibin; cancer;  
 KW nervous system disease; neuropathy; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease; spinal cord disorder;  
 KW head trauma; stroke; myeloid cell disorder; lymphoid cell disorder;  
 KW platelet disorder; thrombocytopaenia; stem cell disorder;  
 KW aplastic anaemia; tissue regeneration; wound healing; ulcer;  
 KW osteoporosis; osteoarthritis; bone degenerative disorder;  
 KW periodontal disease; fibrosis; reperfusion; immune disorder; SCID;  
 KW severe combined immunodeficiency; infection; autoimmune disorder;  
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; allergy;  
 KW asthma; coagulation disorder; haemophilia; sepsis; nephritis;  
 KW inflammatory bowel disease; food supplement; immunogen.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200175093-A1.  
 XX  
 PD 11-OCT-2001.  
 XX  
 PF 30-MAR-2001; 2001WO-US010484.  
 XX  
 PR 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00643167.  
 PR 22-SEP-2000; 2000US-00668680.  
 PR 23-OCT-2000; 2000US-00695618.  
 PR 30-NOV-2000; 2000US-00728711.  
 PR 14-MAR-2001; 2001US-00808701.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Asundi V, Zhou P, Xue AJ, Ren F, Zhang J, Wang J;  
 PI Xu C, Yang Y, Zhao QA, Chen R, Wang D, Goodrich RW, Liu C;  
 PI Drmanac RT;  
 XX  
 DR WPI; 2001-626432/72.  
 DR N-PSDB; AAS59848.  
 XX  
 PT New polypeptides and nucleic acids, useful for diagnosis, treatment of

PT inflammatory, autoimmune, neurological, myeloid or lymphoid cell, bone  
XX degenerative disorders, cancer and promoting wound healing.  
PS Claim 20; Page 279-280; 336pp; English.

XX The invention relates to isolated human polypeptides (which may be  
CC cytokines) and the polynucleotides encoding them. The protein is useful  
CC for identifying a compound which binds to it (e.g. modulators, agonists  
CC and antagonists). The polynucleotides are useful as an array for mismatch  
CC detection. The proteins and nucleic acids are useful as nutritional  
CC sources or supplements. The protein exhibits activity relating  
CC to cytokine, cell proliferation, cell differentiation, antiinflammatory,  
CC stem cell growth factor activity, immune stimulating or immune  
CC suppressing and activin or inhibin related activities. The proteins (and  
CC antibodies raised against them) and nucleic acids are therefore useful in  
CC the diagnosis and treatment of diseases and disorders such as cancer,  
CC central and peripheral nervous system diseases and neuropathies,  
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic  
CC lateral sclerosis, spinal cord disorders, head trauma, cerebrovascular  
CC diseases, stroke, myeloid or lymphoid cell disorders, platelet disorders,  
CC thrombocytopaenia, stem cell disorders, aplastic anaemia, for  
CC regeneration of bone, cartilage, tendon, ligament and/or nerve tissue  
CC growth, and in tissue repair, healing of burns, incisions, ulcers, for  
CC treating osteoporosis, osteoarthritis, bone degenerative disorders, or  
CC periodontal disease, lung or liver fibrosis, reperfusion injury in  
CC various tissues, various immune deficiencies and disorders including  
CC severe combined immunodeficiency (SCID), bacterial or fungal infections,  
CC autoimmune disorders (e.g. multiple sclerosis, rheumatoid arthritis,  
CC diabetes mellitus, myasthenia gravis), allergic reactions and conditions,  
CC such as asthma or other respiratory problems, coagulation disorders,  
CC haemophilia, septic shock, sepsis, arthritis, nephritis and inflammatory  
CC bowel disease, viral infection and are useful in altering bodily  
CC characteristics. The present sequence represents a novel protein of the  
XX invention

XX Sequence 699 AA;

Query Match 63.2%; Score 449; DB 4; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 224 DSEACAESEGLMPQGFLLDFSVDEVAQLTLDLELFSKVRLYECGLSVMSQDRPG 283  
Db 229 DSEACAESEGLMPQGFLLDFSVDEVAQLTLDLELFSKVRLYECGLSVMSQDRPG 288  
QY 284 AAGASPTVATVAQFNVTGCVLGSVLGAPGLAQAQAQRLKRWIRIAQRCRELNFSSL 343  
Db 289 AAGASPTVATVAQFNVTGCVLGSVLGAPGLAQAQAQRLKRWIRIAQRCRELNFSSL 348  
QY 344 RAILSALQSNPIYRLKRSWAGVREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ 403  
Db 349 RAILSALQSNPIYRLKRSWAGVREPLSTFRKLSQIFSDENNHLSSREILFQEEATEGSQ 408  
QY 404 EEDNTGSLSPKPPGPPVPLGTFLTDLVMLDTPALDMLDGLINFEKRRKEWEILLARIQ 463  
Db 409 EEDNTGSLSPKPPGPPVPLGTFLTDLVMLDTPALDMLDGLINFEKRRKEWEILLARIQ 468  
QY 464 QLQRRCOSYTLSPHPPTLAAHQAQNLTEQSVRLSRVIEPPPAACSPSSPRIRRISLTQ 523  
Db 469 QLQRRCOSYTLSPHPPTLAAHQAQNLTEQSVRLSRVIEPPPAACSPSSPRIRRISLTQ 528  
QY 524 RLSAKLAREKSSPGSGPSPSTSSVSPGSPSSPRSDAPAGSPASPSPGQFSTKL 593  
Db 529 RLSAKLAREKSSPGSGPSPSTSSVSPGSPSSPRSDAPAGSPASPSPGQFSTKL 598  
QY 584 PLSLDLPPSPFPALPLGSPRIPLPAQOSSEARVIRSIDNDHGNLYRSILLTSQDKAPSV 643  
Db 589 PLSLDLPPSPFPALPLGSPRIPLPAQOSSEARVIRSIDNDHGNLYRSILLTSQDKAPSV 648  
QY 644 VRRALQKHNVQPWACDYQLFVLPGDRV 672  
Db 649 VRRALQKHNVQPWACDYQLFVLPGDRV 677

## RESULT 7

AED08222  
ID AED08222 standard; protein; 699 AA.

XX AC AED08222;

XX 17-NOV-2005 (first entry)

XX Mouse RalGDS-like protein 3 SEQ ID NO: 86.

XX Immune stimulation; gene therapy; drug screening; transgenic animal;  
KW food; inflammation; antiinflammatory; autoimmune disease;  
KW immunosuppressive; immune disorder; autonomic nervous system disease;  
KW cns-gen.; neurological disease; central nervous system disease; leukemia;  
KW cytostatic; hematological disease; neoplasm; RalGDS-like protein 3.  
XX Mus musculus.

XX US2005202422-A1.

PD 15-SEP-2005.

XX 08-NOV-2002; 2002US-00291128.

XX 31-MAR-2000; 2000US-00540217.

PR 30-MAR-2001; 2001WO-US010484.

XX (TANG/) TANG Y T.

PA (LIUC/) LIU C.

PA (ASUN/) ASUNDI V.

PA (CHEN/) CHEN R.

PA (REN/) REN F.

PA (WANG/) WANG D.

PA (WANG/) WANG J.

PA (XUE/) XUE A J.

PA (YANG/) YANG Y.

PA (ZHAN/) ZHANG J.

PA (ZHAO/) ZHAO Q A.

PA (ZHOU/) ZHOU P.

PA (GOOD/) GOODRICH R W.

PA (DRMA/) DRMANAC R T.

XX Tang YT, Liu C, Asundi V, Chen R, Ren F, Wang D, Wang J, Xu C,  
PI Xue AJ, Yang Y, Zhang J, Zhao QA, Zhou P, Goodrich RW, Drmanac RT;

XX WPI; 2005-618089/63.

DR N-PSDB; AED08179.

XX New isolated polynucleotides, useful for treating, preventing, or  
PT ameliorating, e.g. Alzheimer's disease, Parkinson's disease, Huntington's  
PT disease, amyotrophic lateral sclerosis, or leukemia.

XX Claim 20; SEQ ID NO 86; 60pp; English.

CC The invention relates to polynucleotides and polypeptides capable of  
CC inducing an immune response. The polynucleotides and proteins are useful  
CC for treating, preventing or ameliorating a medical condition, e.g.  
CC Alzheimer's disease, Parkinson's disease, Huntington's disease, the  
CC amyotrophic lateral sclerosis, Shy-Drager syndrome or stroke. The  
CC proteins can be used for treating leukemia, inflammatory arthritis,  
CC autoimmune disorders, e.g. multiple sclerosis, rheumatoid arthritis,  
CC diabetes, myasthenia gravis or autoimmune inflammatory eye disease. They  
CC can also be used as nutritional sources and supplements, e.g. as a carbon  
CC source, nitrogen source or carbohydrate source. The sequences of the  
CC invention are also useful in gene therapy, drug screening and in  
CC production of transgenic animals. The present sequence is the mouse  
CC RalGDS-like protein 3 of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification, but was obtained  
CC in electronic format directly from USPTO at  
CC seqdata.uspto.gov/sequence.html?DocID=20050202422.

XX



SQ Sequence 699 AA;  
 Query Match 63.2%; Score 449; DB 9; Length 699;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DSSACAEELGMPQGLDQFVDEVAEQLTLDLELFKVRLEYCLGVSQDRPG 283  
 DB 229 DSSACAEELGMPQGLDQFVDEVAEQLTLDLELFKVRLEYCLGVSQDRPG 288  
 QY 284 AAGASPTVRATVAQNTVTCVGLSVLGAAPQRAQLEKWIIRIAQRCRELNFSS 343  
 DB 289 AAGASPTVRATVAQNTVTCVGLSVLGAAPQRAQLEKWIIRIAQRCRELNFSS 348  
 QY 344 RAILSALQSNPIYRLKRSWGVSRPLSTFRKLSQIFSDENNHLSSREILFQEEATGSG 403  
 DB 349 RAILSALQSNPIYRLKRSWGVSRPLSTFRKLSQIFSDENNHLSSREILFQEEATGSG 408  
 QY 404 EEDNTPGSLPSKPPGVPVYLGTLTDLVMDLTALPDMLEGLINFKEKRWKEWILARIO 463  
 DB 409 EEDNTPGSLPSKPPGVPVYLGTLTDLVMDLTALPDMLEGLINFKEKRWKEWILARIO 468  
 QY 464 QLRRCOSYTLSPHPPIAALHAQNLTEEQSYRLSVIEPPAASCPSRRIRRIISLTK 523  
 DB 469 QLRRCOSYTLSPHPPIAALHAQNLTEEQSYRLSVIEPPAASCPSRRIRRIISLTK 528  
 QY 524 RLSAKLAREKSSSPGSGPDPSTSSVSPGSPSRSDAPAGSPGPGPSTKL 583  
 DB 529 RLSAKLAREKSSSPGSGPDPSTSSVSPGSPSRSDAPAGSPGPGPSTKL 588  
 QY 584 PLSLDLSPRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 643  
 DB 589 PLSLDLSPRPFALPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSV 648  
 QY 644 VRRALQKHNPQWACDYQLFQVLPQDRV 672  
 DB 649 VRRALQKHNPQWACDYQLFQVLPQDRV 677

RESULT 8  
 ADA55391 standard; protein; 464 AA.  
 AC ADA55391;  
 DT 20-NOV-2003 (first entry)  
 XX Human protein, SEQ ID 2959.  
 DE Cytostatic; Anti-inflammatory; Osteopathic; Neuroprotective; Nootropic;  
 KW Gene Therapy; human; secretory protein; membrane proteins; cancer;  
 KW inflammatory disease; osteoporosis; neurological disease.  
 OS Homo sapiens.  
 XX  
 XX EP1293569-A2.  
 XX  
 XX 19-MAR-2003.  
 XX  
 XX 21-MAR-2002; 2002EP-00006586.  
 XX  
 XX 14-SEP-2001; 2001JP-00328381.  
 PR 24-JAN-2002; 2002US-0350435P.  
 XX  
 XX (HELI-) HELIX RES INST.  
 PA (REAS-) RES ASSOC BIOTECHNOLOGY.  
 XX  
 XX Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
 PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
 PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;  
 XX  
 XX WPI; 2003-395539/38.  
 DR N-PSDB; ADA53752.  
 XX

XX New polynucleotides encoding full-length polypeptides, e.g. secretory  
 PT and/or membrane proteins, useful for developing medicines for diseases in  
 PT which the gene is involved, or as target molecules for gene therapy.  
 XX  
 PS Claim 14; SEQ ID NO 2959; 205pp; English.  
 CC The present invention relates to novel human secretory or membrane  
 CC proteins (ADA54072-ADA55710) and their coding sequences (ADA52433-  
 CC ADA54071). The coding sequences are useful in the gene therapy of  
 CC diseases caused by abnormalities of the proteins, e.g. cancer,  
 CC inflammatory diseases, osteoporosis or neurological disease.  
 XX  
 SQ Sequence 464 AA;  
 Query Match 61.3%; Score 435; DB 6; Length 464;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 435; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 MPOGPQLDQFVDEVAEQLTLDLELFKVRLEYCLGVSQDRPGAGASPTVRATVA 296  
 DB 1 MPOGPQLDQFVDEVAEQLTLDLELFKVRLEYCLGVSQDRPGAGASPTVRATVA 60  
 QY 297 QFNTVTGCVLGSVLGAPGLAAPQRAQLEKWIIRIAQRCRELNFSSRLAISALQSNPIY 356  
 DB 61 QFNTVTGCVLGSVLGAPGLAAPQRAQLEKWIIRIAQRCRELNFSSRLAISALQSNPIY 120  
 QY 357 RLKRSWGVSRPLSTFRKLSQIFSDENNHLSSREILFQEEATGSGEEDNTPGSLPSKP 416  
 DB 121 RLKRSWGVSRPLSTFRKLSQIFSDENNHLSSREILFQEEATGSGEEDNTPGSLPSKP 180  
 QY 417 PPGPVYLGTLTDLVMDLTALPDMLEGLINFKEKRWKEWILARIOQLQRRCOSYTLSP 476  
 DB 181 PPGPVYLGTLTDLVMDLTALPDMLEGLINFKEKRWKEWILARIOQLQRRCOSYTLSP 240  
 QY 477 HPPILAALHAQNLTEEQSYRLSVIEPPAASCPSRRIRRIISLTKRLSAKLAREKSSS 536  
 DB 241 HPPILAALHAQNLTEEQSYRLSVIEPPAASCPSRRIRRIISLTKRLSAKLAREKSSS 300  
 QY 537 PGGSGDPSPSTSSVSPGSPSRSDAPAGSPGPGPSTKLPLSLDLSPRPF 596  
 DB 301 PGGSGDPSPSTSSVSPGSPSRSDAPAGSPGPGPSTKLPLSLDLSPRPF 360  
 QY 597 LPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVRRALQKHNPQ 656  
 DB 361 LPLGSPRIPLPAQSSSEARVIRVSDNDHGNLYRSILLTSQDKAPSVRRALQKHNPQ 420  
 QY 657 WACDYQLFQVLPQDR 671  
 DB 421 WACDYQLFQVLPQDR 435

RESULT 9  
 ABR41327  
 ID ABR41327 standard; protein; 562 AA.  
 XX  
 XX ABR41327;  
 XX  
 XX 02-JUN-2003 (first entry)  
 XX Human DITHP intracellular signalling protein.  
 DE Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;  
 KW cancer; cell proliferative disorder; autoimmune disorder;  
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;  
 KW neurological disorder; gastrointestinal disorder; transport disorder;  
 KW connective tissue disorder; drug screening; proteome analysis;  
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;  
 KW disease model; toxicological testing; transcript imaging;  
 KW intracellular signalling.  
 XX  
 XX Homo sapiens.  
 OS



FN WO200297031-A2.  
 XX 05-DEC-2002.  
 XX 27-MAR-2002; 2002WO-US010056.  
 XX 28-MAR-2001; 2001US-0279619P.  
 PR 29-MAR-2001; 2001US-0280067P.  
 PR 29-MAR-2001; 2001US-0280068P.  
 PR 16-MAY-2001; 2001US-0291280P.  
 PR 17-MAY-2001; 2001US-0291829P.  
 PR 17-MAY-2001; 2001US-0291849P.  
 PR 19-JUN-2001; 2001US-0299428P.  
 PR 20-JUN-2001; 2001US-0299776P.  
 PR 20-JUN-2001; 2001US-0300001P.  
 XX (INCY-) INCYTE GENOMICS INC.  
 PA Dafo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;  
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstein EH;  
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
 XX WPI; 2003-129518/12.  
 DR N-PSDB; ACC46267.  
 XX Novel human diagnostic and therapeutic polypeptide useful for identifying  
 PT test compound which specifically binds to a polypeptide encoded by human  
 FT diagnostic and therapeutic polynucleotide, and to induce antibodies.  
 XX Claim 27; SEQ ID NO 862; 591pp; English.  
 XX The invention relates to novel human diagnostic and therapeutic  
 CC polynucleotides designated dithp (ACC4680-ACC46749) and to their encoded  
 CC proteins (DITHP; ABK41136-ABK41812). The invention also relates to  
 CC polynucleotide sequences at least 90% identical to the dithp cDNA  
 CC sequences of the invention; recombinant vectors, host cells and  
 CC transgenic organisms comprising a dithp nucleic acid sequence; the  
 CC recombinant production of DITHP proteins; antibodies specific for DITHP  
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods of  
 CC detecting dithp nucleotide and protein sequences; methods of screening  
 CC for compounds which specifically bind a DITHP protein; and methods of  
 CC assessing the toxicity of test compounds using a dithp hybridisation  
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the  
 CC diagnosis of a wide variety of conditions including cancer and other cell  
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,  
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic  
 CC disorders; neurological disorders; gastrointestinal disorders; transport  
 CC disorders; and connective tissue disorders. They may also be used to  
 CC screen for modulators of protein activity or gene expression. DITHP  
 CC proteins can additionally be used in analysis of the proteome of a tissue  
 CC or cell type and to induce antibodies. The dithp nucleic acids are  
 CC additionally useful in somatic or germline gene therapy of the disorders  
 CC mentioned above, as a source of antisense sequences, as a source of  
 CC probes and primers, in genotyping and identification of individuals, in  
 CC the generation of transgenic animal models of human disease or knock in  
 CC humanised animals, in toxicological testing, and in transcript imaging.  
 CC The present sequence represents a DITHP protein which has intracellular  
 CC signalling activity. Note: The sequence data for this patent did not form  
 CC part of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 562 AA;  
 SQ  
 Query Match 54.1%; Score 384; DB 6; Length 562;  
 Best Local Similarity 99.8%; Pred. NO. 0;  
 Matches 484; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 187 KAEKLEDFLEAREEQEERPPQVWTGPPRVAOTSDPDSSACAEFEELGMPQGLDFF 246  
 DB 52 KAEKLEDFLEAREEQEERPPQVWTGPPRVAOTSDPDSSACAEFEELGMPQGLDFF 111

247 SVDEVAEQTLIDLELFSKVRLYECLGSVMSQDRPGAGASPTVRATVATQFNTVTGCVL 306  
 DB 112 SVDEVAEQTLIDLELFSKVRLYECLGSVMSQDRPGAGASPTVRATVATQFNTVTGCVL 171  
 QY 307 GSVLGAPGLAAPORAQRLKWIIRIAQRCRELRFSSRLRAILSALQSNPIYRLKRSWAGVS 366  
 DB 172 GSVLGAPGLAAPORAQRLKWIIRIAQRCRELRFSSRLRAILSALQSNPIYRLKRSWAGVS 231  
 QY 367 REPLSTFKLSQJFSFSDNNHLSREILFQEEATEGSEEDNTPGSLSPKPPGPPVPLGT 426  
 DB 232 REPLSTFKLSQJFSFSDNNHLSREILFQEEATEGSEEDNTPGSLSPKPPGPPVPLGT 291  
 QY 427 FLTDVLMDTALPDMLEGLINFEXKRWKEWIIARIQQLQRRQSYTLSPHPPIAALHA 486  
 DB 292 FLTDVLMDTALPDMLEGLINFEXKRWKEWIIARIQQLQRRQSYTLSPHPPIAALHA 351  
 QY 487 QNOLTEQSYRLSRVIEPPPAASCPSPIRRIRSLTKRLSAKLAREKSSPSGDPSS 546  
 DB 352 QNOLTEQSYRLSRVIEPPPAASCPSPIRRIRSLTKRLSAKLAREKSSPSGDPSS 411  
 QY 547 PTSSVSPGSPSPSRSDAPAGSPGPGSTKLPLSLDLPSPPRFPALPLGSPRIPL 606  
 DB 412 PTSSVSPGSPSPSRSDAPAGSPGPGSTKLPLSLDLPSPPRFPALPLGSPRIPL 471  
 QY 607 PAQCSSEARVIRVSIIDNHGNYLSILLTSQDKAPSVVRALQKHNVPQPMACDYQLFQV 666  
 DB 472 PAQCSSEARVIRVSIIDNHGNYLSILLTSQDKAPSVVRALQKHNVPQPMACDYQLFQV 531  
 QY 667 LPGDR 671  
 DB 532 LPGDR 536

RESULT 10  
 ABO15021  
 ID ABO15021 standard; protein; 708 AA.  
 XX AC ABO15021;  
 XX DT 26-AUG-2003 (first entry)  
 XX DE Human NOV24 protein.  
 XX Human; NOVX; inflammatory disorder; demyelination disease; stroke;  
 KW renal disorder; infection; cardiomyopathy; atherosclerosis; acne;  
 KW hypertension; pancreatitis; Von Hippel-Lindau; endometriosis; fertility;  
 KW scleroderma; cirrhosis; inflammatory bowel disease; Crohn's disease;  
 KW haemophilia; autoimmune disease; allergy; AIDS;  
 KW graft versus host disease; Alzheimer's disease; arthritis; pain;  
 KW Parkinson's disease; Huntington's disease; obesity; diabetes;  
 KW hair growth; hair loss; asthma; schizophrenia; glomerulonephritis;  
 KW lupus erythematosus; psoriasis; antidiabetic; anorectic; metabolic;  
 KW neuroprotection; cytotaxtic; antihypertensive; cerebroprotective;  
 KW prothrombotic; antiarteriosclerotic; hypotensive; cerebroprotective;  
 KW antiinflammatory; gynaecological; antifertility; dermatological;  
 KW hepatocellular; haemostatic; immunosuppressive; antiallergic;  
 KW antiarthritic; anticonvulsant; antiseborrhoeic; antiaschemic;  
 KW neuroleptic; anti-HIV; analgesic; nephrotropic; antipsoriatic.  
 XX Homo sapiens.  
 OS  
 XX WC200298917-A2.  
 PN  
 XX 12-DEC-2002.  
 XX 12-FEB-2002; 2002WO-US022049.  
 XX 12-FEB-2001; 2001US-0268221P.  
 PR 13-FEB-2001; 2001US-0268496P.  
 PR 14-FEB-2001; 2001US-0268646P.  
 PR 14-FEB-2001; 2001US-0268665P.  
 PR 15-FEB-2001; 2001US-0269136P.  
 PR 16-FEB-2001; 2001US-0269310P.



Db 1 MPQGPQLLDFSVDEVAEQTLTDLIDLEFSKVRLYECLGWSQDRPFGAAGASPTVRATVA 60  
QY 297 QNTVTGCVLGSVLGAPGLAAPQRAQRLKWKIRIAQRCRELNFSSRLAILLSALQSNPIY 356  
Db 61 QNTVTGCVLGSVLGAPGLAAPQRAQRLKWKIRIAQRCRELNFSSRLAILLSALQSNPIY 120  
QY 357 RLKRSWGAVEREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSOEDNTPGSLPSKP 416  
Db 121 RLKRSWGAVEREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSOEDNTPGSLPSKP 180  
QY 417 PPGVPVYLGTFLTDLVMLDTPDMLE 443  
Db 181 PPGVPVYLGTFLTDLVMLDTPDMLE 207

## RESULT 12

AM20233  
ID AEC88198 standard; protein; 208 AA.

XX AC AEC88198;

XX DT 01-DEC-2005 (first entry)

XX XX Human cDNA clone protein PROSTR20161950, SEQ ID 3953.

XX DE Osteopathic; Cytostatic; Antiinflammatory; Gastrointestinal-Gen.;  
KW Antulcer; Gene Therapy; Osteoporosis; cancer; inflammation; gastritis;  
KW stomach ulcer; gastrointestinal ulcer.

XX OS Homo sapiens.

XX XX EP1580263-A1.

XX PD 28-SEP-2005.

XX PF 12-APR-2002; 2004EP-00027348.

XX PR 22-MAR-2002; 2002JP-00137785.

XX PR 12-APR-2002; 2002EP-00008400.

XX PA (REAS-) RES ASSOC BIOTECHNOLOGY.

XX PI Isogai T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ishii S;  
PI Yamamoto J, Isono Y, Hio Y, Otsuka K, Nagai K, Irie R, Tamechika I;  
PI Seki N, Yoshikawa T, Otsuka M, Nagahari K, Masuho Y;

XX DR WPI; 2005-667421/69.

XX DR N-PSDB; AEC85755.

XX PT New full-length cDNA sequences, useful for treating diseases, e.g.

XX PT osteoporosis, cancer, inflammation, gastritis, or gastroduodenal ulcer.

XX PS Example 3; SEQ ID NO 3953; 296pp; English.

XX CC The present invention relates to novel human cDNAs (AEC84246-AEC86688)  
CC encoding proteins AEC86689-AEC89131. The cDNAs are useful for analyzing  
CC the functions of the proteins, and for developing medicines for diseases  
CC e.g. osteoporosis, cancer, inflammation, gastritis, or gastroduodenal  
CC ulcer. Note: The sequence data for this patent did not form part of the  
CC printed specification but was obtained in electronic format directly from  
CC EPO.

XX XX Sequence 208 AA;

Query Match 29.2%; Score 207; DB 9; Length 208;

Best Local Similarity 100.0%; Pred. No. 4.9e-188;

Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 MPQGPQLLDFSVDEVAEQTLTDLIDLEFSKVRLYECLGWSQDRPFGAAGASPTVRATVA 296  
Db 1 MPQGPQLLDFSVDEVAEQTLTDLIDLEFSKVRLYECLGWSQDRPFGAAGASPTVRATVA 60

QY 297 QNTVTGCVLGSVLGAPGLAAPQRAQRLKWKIRIAQRCRELNFSSRLAILLSALQSNPIY 356

Db 61 QNTVTGCVLGSVLGAPGLAAPQRAQRLKWKIRIAQRCRELNFSSRLAILLSALQSNPIY 120  
QY 357 RLKRSWGAVEREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSOEDNTPGSLPSKP 416  
Db 121 RLKRSWGAVEREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSOEDNTPGSLPSKP 180  
QY 417 PPGVPVYLGTFLTDLVMLDTPDMLE 443  
Db 181 PPGVPVYLGTFLTDLVMLDTPDMLE 207

## RESULT 13

AM20233

ID AM20233 standard; protein; 70 AA.

XX AC AM20233;

XX DT 12-OCT-2001 (first entry)

XX DE Peptide #6667 encoded by probe for measuring cervical gene expression.

XX KW Probe; human; microarray; gene expression; cervical epithelial cell;

XX KW cervical cancer.

XX OS Homo sapiens.

XX XX WO200157278-A2.

XX PD 09-AUG-2001.

XX PF 30-JAN-2001; 2001WO-US000670.

XX PR 04-FEB-2000; 2000US-0180312P.

XX PR 26-MAY-2000; 2000US-0207456P.

XX PR 30-JUN-2000; 2000US-00608408.

XX PR 03-AUG-2000; 2000US-00632366.

XX PR 21-SEP-2000; 2000US-0234687P.

XX PR 27-SEP-2000; 2000US-0236359P.

XX PR 04-OCT-2000; 2000GB-00024263.

XX PA (MOLE-) MOLECULAR DYNAMICS INC.

XX PI Penn SG, Hanzel DK, Chen W, Rank DR;

XX DR WPI; 2001-488901/53.

XX XX Human genome-derived single exon nucleic acid probes useful for analyzing  
XX PT gene expression in human cervical epithelial cells.

XX PS Claim 27; SEQ ID NO 25059; 487pp; English.

XX CC The present invention relates to human single exon nucleic acid probes  
CC (SENPs; see AAI10068-AA128459). The present sequence is a peptide encoded  
CC by one such probe. The SENPs are derived from human Hela cells. The SENPs  
CC can be used to produce a single exon microarray, which can be used for  
CC measuring human gene expression in a sample derived from human cervical  
CC epithelial cells. By measuring gene expression, the probes are therefore  
CC useful in grading and/or staging of diseases of the cervix, notably  
CC cervical cancer. Note: The sequence data for this patent did not form  
CC part of the printed specification, but was obtained in electronic format  
CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences

XX XX Sequence 70 AA;

Query Match 6.8%; Score 48; DB 4; Length 70;

Best Local Similarity 100.0%; Pred. No. 4.8e-37;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 165 HSDLGSVRTFLGWAAPGSAEAKAEKLEDFLEAREQEPEEPQVWT 212

Db 23 HSDLGSVRTFLGWAAPGSAEAKAEKLEDFLEAREQEPEEPQVWT 70

```

RESULT 14
ABB40566
ID  ABB40566 standard; peptide; 70 AA.
XX  AC
XX  ABB40566;
XX  DT
XX  04-FEB-2002 (first entry)
XX  DE
XX  Peptide #8072 encoded by human foetal liver single exon probe.
XX  KW
XX  Human; foetal liver; gene expression; single exon nucleic acid probe.
XX  OS
XX  Homo sapiens.
XX  PN
XX  WO200157277-A2.
XX  PD
XX  09-AUG-2001.
XX  PF
XX  30-JAN-2001; 2001WO-US000669.
XX  PR
XX  04-FEB-2000; 2000US-0180312P.
XX  PR
XX  26-MAY-2000; 2000US-0207456P.
XX  PR
XX  30-JUN-2000; 2000US-00608408.
XX  PR
XX  03-AUG-2000; 2000US-00632366.
XX  PR
XX  21-SEP-2000; 2000US-0234687P.
XX  PR
XX  27-SEP-2000; 2000US-0236359P.
XX  PR
XX  04-OCT-2000; 2000GB-00024263.
XX  PA
XX  (MOLE-) MOLECULAR DYNAMICS INC.
XX  PI
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
XX  WPI; 2001-483447/52.
XX  PT
XX  Human genome-derived single exon nucleic acid probes useful for analyzing
XX  gene expression in human fetal liver.
XX  PS
XX  Claim 27; SEQ ID NO 33201; 639pp + Sequence Listing; English.
XX  CC
XX  The invention relates to a single exon nucleic acid probe for measuring
XX  human gene expression in a sample derived from human foetal liver. The
XX  single exon nucleic acid probes may be used for predicting, measuring and
XX  displaying gene expression in samples derived from human fetal liver. The
XX  present invention is a peptide encoded by a single exon nucleic acid probe
XX  of the invention. Note: The sequence data for this patent did not form
XX  part of the printed specification, but was obtained in electronic format
XX  directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX  SQ
XX  Sequence 70 AA;
XX  Query Match 6.8%; Score 48; DB 4; Length 70;
XX  Best Local Similarity 100.0%; Pred. No. 4.8e-37;
XX  Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  QY
XX  165 HSDLGSVRTFLGWAAPGSAEAKKLEDFLEAEAEQEEPPQVWT 212
XX  Db
XX  23 HSDLGSVRTFLGWAAPGSAEAKKLEDFLEAEAEQEEPPQVWT 70

RESULT 15
AAM34328
ID  AAM34328 standard; protein; 70 AA.
XX  AC
XX  AAM34328;
XX  DT
XX  17-OCT-2001 (first entry)
XX  DE
XX  Peptide #8365 encoded by probe for measuring placental gene expression.
XX  KW
XX  Probe; microarray; human; placenta; antenatal diagnosis;
XX  genetic disorder.

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OS  Homo sapiens.
XX  WO200157272-A2.
XX  PD
XX  09-AUG-2001.
XX  PF
XX  30-JAN-2001; 2001WO-US000663.
XX  PR
XX  04-FEB-2000; 2000US-0180312P.
XX  PR
XX  26-MAY-2000; 2000US-0207456P.
XX  PR
XX  30-JUN-2000; 2000US-00608408.
XX  PR
XX  03-AUG-2000; 2000US-00632366.
XX  PR
XX  21-SEP-2000; 2000US-0234687P.
XX  PR
XX  27-SEP-2000; 2000US-0236359P.
XX  PR
XX  04-OCT-2000; 2000GB-00024263.
XX  PA
XX  (MOLE-) MOLECULAR DYNAMICS INC.
XX  PI
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
XX  WPI; 2001-488897/53.
XX  DR
XX  Human genome-derived single exon nucleic acid probes useful for analyzing
XX  gene expression in human placenta.
XX  PS
XX  Claim 27; SEQ ID NO 34597; 654pp; English.
XX  CC
XX  The present invention relates to single exon nucleic acid probes (SENP:
XX  see AAI31315-AAI57546). The present sequence is a peptide encoded by one
XX  such probe. The probes are useful for producing a microarray for
XX  predicting, measuring and displaying gene expression in samples derived
XX  from human placenta. The probes are useful for antenatal diagnosis of
XX  human genetic disorders
XX  SQ
XX  Sequence 70 AA;
XX  Query Match 6.8%; Score 48; DB 4; Length 70;
XX  Best Local Similarity 100.0%; Pred. No. 4.8e-37;
XX  Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX  QY
XX  165 HSDLGSVRTFLGWAAPGSAEAKKLEDFLEAEAEQEEPPQVWT 212
XX  Db
XX  23 HSDLGSVRTFLGWAAPGSAEAKKLEDFLEAEAEQEEPPQVWT 70

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GenCore version 5.1.9  
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Title: US-10-694-438-2  
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Maximum DB seq length: 2000000000

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID                  | Description        |
|------------|-------|-------------|--------|----|---------------------|--------------------|
| 1          | 710   | 100.0       | 710    | 2  | US-10-118-328-2     | Sequence 2, Appli  |
| 2          | 487   | 68.6        | 715    | 2  | US-09-808-701A-33   | Sequence 33, Appli |
| 3          | 449   | 63.2        | 699    | 2  | US-09-808-701A-34   | Sequence 34, Appli |
| 4          | 435   | 61.3        | 464    | 2  | US-10-094-749-2959  | Sequence 2959, Ap  |
| 5          | 47    | 6.6         | 709    | 2  | US-10-118-328-4     | Sequence 4, Appli  |
| 6          | 17    | 2.4         | 852    | 1  | US-08-408-519-5     | Sequence 5, Appli  |
| 7          | 17    | 2.4         | 852    | 5  | PCT-US95-03552-5    | Sequence 5, Appli  |
| 8          | 11    | 1.5         | 378    | 2  | US-09-949-016-8733  | Sequence 8733, Ap  |
| 9          | 11    | 1.5         | 725    | 2  | US-10-118-328-5     | Sequence 5, Appli  |
| 10         | 11    | 1.5         | 768    | 1  | US-08-408-519-2     | Sequence 2, Appli  |
| 11         | 11    | 1.5         | 768    | 5  | PCT-US95-03552-2    | Sequence 2, Appli  |
| 12         | 10    | 1.4         | 313    | 2  | US-09-270-767-31859 | Sequence 31859, A  |
| 13         | 10    | 1.4         | 313    | 2  | US-09-270-767-47076 | Sequence 47076, A  |
| 14         | 9     | 1.3         | 122    | 1  | US-08-820-170A-1    | Sequence 1, Appli  |
| 15         | 9     | 1.3         | 122    | 2  | US-09-055-699-1     | Sequence 1, Appli  |
| 16         | 9     | 1.3         | 122    | 2  | US-09-273-565-1     | Sequence 1, Appli  |
| 17         | 9     | 1.3         | 122    | 2  | US-09-565-538-1     | Sequence 1, Appli  |
| 18         | 9     | 1.3         | 122    | 2  | US-09-661-468-1     | Sequence 1, Appli  |
| 19         | 9     | 1.3         | 122    | 2  | US-09-976-165-1     | Sequence 1, Appli  |
| 20         | 9     | 1.3         | 420    | 2  | US-09-902-540-12464 | Sequence 12464, A  |
| 21         | 9     | 1.3         | 502    | 2  | US-09-833-577A-14   | Sequence 14, Appli |
| 22         | 9     | 1.3         | 782    | 2  | US-09-949-016-11571 | Sequence 11571, A  |
| 23         | 8     | 1.1         | 26     | 1  | US-07-942-245-391   | Sequence 391, App  |
| 24         | 8     | 1.1         | 26     | 1  | US-07-808-245-398   | Sequence 398, App  |
| 25         | 8     | 1.1         | 65     | 1  | US-07-808-457-7     | Sequence 7, Appli  |
| 26         | 8     | 1.1         | 65     | 5  | PCT-US92-10178-7    | Sequence 7, Appli  |

27 8 1.1 77 2 US-09-621-976-4540 Sequence 4540, Ap  
28 8 1.1 91 1 US-07-808-457-11 Sequence 11, Appl  
29 8 1.1 91 5 PCT-US92-10178-11 Sequence 11, Appl  
30 8 1.1 139 1 US-07-808-457-13 Sequence 13, Appl  
31 8 1.1 139 5 PCT-US92-10178-13 Sequence 13, Appl  
32 8 1.1 139 5 PCT-US92-10178-13 Sequence 13, Appl  
33 8 1.1 149 1 US-07-808-457-15 Sequence 15, Appl  
34 8 1.1 149 2 PCT-US92-10178-15 Sequence 15, Appl  
35 8 1.1 149 5 PCT-US92-10178-15 Sequence 15, Appl  
36 8 1.1 150 1 US-07-808-457-17 Sequence 17, Appl  
37 8 1.1 150 5 PCT-US92-10178-17 Sequence 17, Appl  
38 8 1.1 155 2 US-09-252-991A-17954 Sequence 17954, A  
39 8 1.1 161 2 US-09-252-991A-27639 Sequence 27639, A  
40 8 1.1 164 1 US-07-808-457-19 Sequence 19, Appl  
41 8 1.1 164 5 PCT-US92-10178-19 Sequence 19, Appl  
42 8 1.1 197 2 US-09-252-991A-26537 Sequence 26537, A  
43 8 1.1 200 1 US-08-170-596-15 Sequence 15, Appl  
44 8 1.1 214 2 US-09-252-991A-24236 Sequence 24236, A  
45 8 1.1 240 7 5204445-2 Patent No. 5204445  
266 1 US-07-808-457-3 Sequence 3, Appli

## ALIGNMENTS

RESULT 1  
US-10-118-328-2  
; Sequence 2, Application US/10118328  
; Patent No. 6773904  
; GENERAL INFORMATION:  
; APPLICANT: YAN, Chunhua et al.  
; TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE  
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF  
; FILE REFERENCE: CLO01220  
; CURRENT APPLICATION NUMBER: US/10/118,328  
; CURRENT FILING DATE: 2002-04-09  
; PRIOR APPLICATION NUMBER: 60/282,460  
; PRIOR FILING DATE: 2001-04-10  
; NUMBER OF SEQ ID NOS: 5  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 710  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-118-328-2

Query Match 100.0%; Score 710; DB 2; Length 710;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 710; Conservative, 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MERTAGKELALAPLDQWGEETEDGAVYSVLSRRORSRSPAEQSGQSPPIANTFLH 60  
QY 61 YRTSKRVLRARLERLVGELVFGDREGDPSFMPAFIATYRTFTVFTACLLGFLPPMPPP 120  
DB 61 YRTSKRVLRARLERLVGELVFGDREGDPSFMPAFIATYRTFTVFTACLLGFLPPMPPP 120  
QY 121 PPPGVEIKTKAVQDLSFNKNLRVAVSVLGSLQDHPDQDRDHPVHSDLSGVRTFLGWAAP 180  
DB 121 PPPGVEIKTKAVQDLSFNKNLRVAVSVLGSLQDHPDQDRDHPVHSDLSGVRTFLGWAAP 180  
QY 181 GSAEAKAEKLLDFLEAEAREQEEPPQVWTGPPRVAQTSDPDSSACAESEGLMPOG 240  
DB 181 GSAEAKAEKLLDFLEAEAREQEEPPQVWTGPPRVAQTSDPDSSACAESEGLMPOG 240  
QY 241 POLLDFSVDEVAEQTLIDLELFSKVLRYECLGVSWSQDRPGAGASPTVRATVAQNT 300  
DB 241 POLLDFSVDEVAEQTLIDLELFSKVLRYECLGVSWSQDRPGAGASPTVRATVAQNT 300  
QY 301 VTGCVLGSVLGAPCLAAPQRAQRLKWKIRTAQRCLRNFSLSRAILSALQSNFIYRLKR 360  
DB 301 VTGCVLGSVLGAPCLAAPQRAQRLKWKIRTAQRCLRNFSLSRAILSALQSNFIYRLKR 360

QY 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSEEDNTPGSLPKPPGP 420  
DB 361 SWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEGSEEDNTPGSLPKPPGP 420  
QY 421 VPYLGTFITDLVMDLTALPDMLEGLINFEKRRKEWEILARIQLOQRCCQSYTILSPHPI 480  
DB 421 VPYLGTFITDLVMDLTALPDMLEGLINFEKRRKEWEILARIQLOQRCCQSYTILSPHPI 480  
QY 481 LAALHAQNOLTEQSYRLSRVIEPPAASCPSPRIIRRIISLTUKLSAKLAREKSSPSGS 540  
DB 481 LAALHAQNOLTEQSYRLSRVIEPPAASCPSPRIIRRIISLTUKLSAKLAREKSSPSGS 540  
QY 541 PGDPSSPTSSVSPGPPSPSRDAPAGSPASPGQPGSTKLPLSLDLPSRPFALPLG 600  
DB 541 PGDPSSPTSSVSPGPPSPSRDAPAGSPASPGQPGSTKLPLSLDLPSRPFALPLG 600  
QY 601 SPRIPPLAQOQSEARVIRVSDNDHGNLYRSILTSQDKAPSVVRRALQKHNVPQWACD 660  
DB 601 SPRIPPLAQOQSEARVIRVSDNDHGNLYRSILTSQDKAPSVVRRALQKHNVPQWACD 660  
QY 661 YQLFQVLPGRVLLIPDNANFYAMSPVAPRDFMLRRKGTNTLSVSPS 710  
DB 661 YQLFQVLPGRVLLIPDNANFYAMSPVAPRDFMLRRKGTNTLSVSPS 710

## RESULT 2

US-09-808-701A-33  
; Sequence 33, Application US/09808701A  
; Patent No. 6610536  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Dmanac, Radoje T.  
; TITLE OF INVENTION: No. 6610536el Nucleic Acids and  
; FILE REFERENCE: 790CIP2D  
; CURRENT APPLICATION NUMBER: US/09/808,701A  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 33  
; LENGTH: 715  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-808-701A-33

Query Match 68.6%; Score 487; DB 2; Length 715;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DSSEACAEEEGLMPQGPOLLDSVDEVAEOLTLDLELFSKVLRYECLGSVMSQDRPG 293  
DB 229 DSSEACAEEEGLMPQGPOLLDSVDEVAEOLTLDLELFSKVLRYECLGSVMSQDRPG 288  
QY 284 AAGASPTVRATVAQNTVTGCVLGSVLGAPGLAAPQRAQLEKWKIRIAQRCRELNFSS 343  
DB 289 AAGASPTVRATVAQNTVTGCVLGSVLGAPGLAAPQRAQLEKWKIRIAQRCRELNFSS 348  
QY 344 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEG 403  
DB 349 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEG 408  
QY 404 EEDNTPGSLPKPPGPVPLGTFTDLVMDLTALPDMLEGLINFEKRRKEWEILARIQ 463  
DB 409 EEDNTPGSLPKPPGPVPLGTFTDLVMDLTALPDMLEGLINFEKRRKEWEILARIQ 468  
QY 464 QLQRCQSYTILSPHPPIAALHAQNOLTEQSYRLSRVIEPPAASCPSPRIIRRIISLT 523

DB 469 QLQRCQSYTILSPHPPIAALHAQNOLTEQSYRLSRVIEPPAASCPSPRIIRRIISLT 528  
QY 524 RLSAKLAREKSSPSGSGDPSPSTSSVSPGSPSRDAPAGSPASPGQPGSTKL 583  
DB 529 RLSAKLAREKSSPSGSGDPSPSTSSVSPGSPSRDAPAGSPASPGQPGSTKL 588  
QY 584 PLSLDLPSPRPFALPLGSPRIPLPAQOQSEARVIRVSDNDHGNLYRSILTSQDKAPSV 643  
DB 589 PLSLDLPSPRPFALPLGSPRIPLPAQOQSEARVIRVSDNDHGNLYRSILTSQDKAPSV 648  
QY 644 VRRALQKHNVPQWACDYQLFQVLPGRVLLIPDNANFYAMSPVAPRDFMLRRKGTNR 703  
DB 649 VRRALQKHNVPQWACDYQLFQVLPGRVLLIPDNANFYAMSPVAPRDFMLRRKGTNR 708  
QY 704 TLSVSPS 710  
DB 709 TLSVSPS 715

## RESULT 3

US-09-808-701A-34  
; Sequence 34, Application US/09808701A  
; Patent No. 6610536  
; GENERAL INFORMATION:  
; APPLICANT: Tang, Y. Tom  
; APPLICANT: Goodrich, Ryle  
; APPLICANT: Asundi, Vinod  
; APPLICANT: Dmanac, Radoje T.  
; TITLE OF INVENTION: No. 6610536el Nucleic Acids and  
; FILE REFERENCE: 790CIP2D  
; CURRENT APPLICATION NUMBER: US/09/808,701A  
; CURRENT FILING DATE: 2002-03-14  
; PRIOR FILING DATE: 2000-08-23  
; PRIOR FILING DATE: 2000-03-31  
; NUMBER OF SEQ ID NOS: 34  
; SOFTWARE: pt\_FL\_genes Version 2.0  
; SEQ ID NO 34  
; LENGTH: 699  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-808-701A-34

Query Match 63.2%; Score 449; DB 2; Length 699;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 449; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DSSEACAEEEGLMPQGPOLLDSVDEVAEOLTLDLELFSKVLRYECLGSVMSQDRPG 293  
DB 229 DSSEACAEEEGLMPQGPOLLDSVDEVAEOLTLDLELFSKVLRYECLGSVMSQDRPG 288  
QY 284 AAGASPTVRATVAQNTVTGCVLGSVLGAPGLAAPQRAQLEKWKIRIAQRCRELNFSS 343  
DB 289 AAGASPTVRATVAQNTVTGCVLGSVLGAPGLAAPQRAQLEKWKIRIAQRCRELNFSS 348  
QY 344 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEG 403  
DB 349 RAILSALQSNPIYRLKRSWGAVSREPLSTFRKLSQIFSDENNHLSSREILFOEATEG 408  
QY 404 EEDNTPGSLPKPPGPVPLGTFTDLVMDLTALPDMLEGLINFEKRRKEWEILARIQ 463  
DB 409 EEDNTPGSLPKPPGPVPLGTFTDLVMDLTALPDMLEGLINFEKRRKEWEILARIQ 468  
QY 464 QLQRCQSYTILSPHPPIAALHAQNOLTEQSYRLSRVIEPPAASCPSPRIIRRIISLT 523  
DB 469 QLQRCQSYTILSPHPPIAALHAQNOLTEQSYRLSRVIEPPAASCPSPRIIRRIISLT 528  
QY 524 RLSAKLAREKSSPSGSGDPSPSTSSVSPGSPSRDAPAGSPASPGQPGSTKL 583  
DB 529 RLSAKLAREKSSPSGSGDPSPSTSSVSPGSPSRDAPAGSPASPGQPGSTKL 588

| Query Match           | 61.3%;          | Score 435;    | DB 2;       | Length 464; |                |                  |                 |           |     |
|-----------------------|-----------------|---------------|-------------|-------------|----------------|------------------|-----------------|-----------|-----|
| Best Local Similarity | 100.0%;         | Pred. No. 0;  |             |             |                |                  |                 |           |     |
| Matches 435;          | Conservative 0; | Mismatches 0; | Indels 0;   | Gaps 0;     |                |                  |                 |           |     |
| QY                    | 237             | MPQGPQLLD     | FSVDEVAEQLT | LDLELFSKVR  | LYECLGSVMSQDRD | FGAAGASPTVRATVA  | 296             |           |     |
| DB                    |                 | 1             | MPQGPQLLD   | FSVDEVAEQLT | LDLELFSKVR     | LYECLGSVMSQDRD   | FGAAGASPTVRATVA | 60        |     |
| QY                    | 297             | QFNTVTGCV     | LSVGLGAPGLA | APQAORLEK   | WIIRIAQRCREL   | NFSSRLRILSALOSNP | 356             |           |     |
| DB                    | 61              | QFNTVTGCV     | LSVGLGAPGLA | APQAORLEK   | WIIRIAQRCREL   | NFSSRLRILSALOSNP | 120             |           |     |
| QY                    | 357             | RLKRSWGA      | VSREPLSTFR  | KLSQLQSF    | DENNHLSSREIL   | FQEEATEGQ        | OEEDNTPGSLPSKP  | 416       |     |
| DB                    | 121             | RLKRSWGA      | VSREPLSTFR  | KLSQLQSF    | DENNHLSSREIL   | FQEEATEGQ        | OEEDNTPGSLPSKP  | 180       |     |
| QY                    | 417             | PPGPVPY       | LGTFLLD     | VMLD        | TALPDL         | EGDILN           | FEKXKKEWELARIQ  | QLQRCCSYT | 476 |
| DB                    | 181             | PPGPVPY       | LGTFLLD     | VMLD        | TALPDL         | EGDILN           | FEKXKKEWELARIQ  | QLQRCCSYT | 240 |
| QY                    | 477             | HPPIIALA      | HAQNOLTEQ   | OSYLSRV     | IEPPAASC       | FPSSPR           | TRRRISLTKRLSA   | KLAAREKSS | 536 |
| DB                    | 241             | HPPIIALA      | HAQNOLTEQ   | OSYLSRV     | IEPPAASC       | FPSSPR           | TRRRISLTKRLSA   | KLAAREKSS | 300 |

RESULT 6  
US-08-408-519-5  
Sequence 5, Application US/08408519  
Patent No. 5955354  
GENERAL INFORMATION:  
APPLICANT: Williams, Lewis T.  
APPLICANT: Demo, Susan  
TITLE OF INVENTION: A No. 5955354el ras p21-Interacting Protein and  
TITLE OF INVENTION: Uses Thereof  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/408,519  
FILING DATE: 20-MAR-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684



REFERENCE/DOCKET NUMBER: 02307K-56800  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 852 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-408-519-5

Query Match 2.4%; Score 17; DB 1; Length 852;  
Best Local Similarity 100.0%; Pred. No. 6.7e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 421 VPYLGTFITDLVMDTA 437  
|||||  
Db 502 VPYLGTFITDLVMDTA 518

## RESULT 7

PCT-US95-03552-5  
Sequence 5, Application PC/TUS9503552  
GENERAL INFORMATION:  
APPLICANT: Williams, Lewis T.  
APPLICANT: Demo, Susan  
TITLE OF INVENTION: A Novel ras p21-Interacting Protein and  
TITLE OF INVENTION: Uses Thereof  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend Khourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/03552  
FILING DATE: 20-MAR-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Dow, Karen B.  
REGISTRATION NUMBER: 29,684  
REFERENCE/DOCKET NUMBER: 02307K-56800  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-326-2400  
TELEFAX: 415-326-2422  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 852 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
PCT-US95-03552-5

Query Match 2.4%; Score 17; DB 5; Length 852;  
Best Local Similarity 100.0%; Pred. No. 6.7e-07;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 421 VPYLGTFITDLVMDTA 437  
|||||  
Db 502 VPYLGTFITDLVMDTA 518

## RESULT 8

Sequence 5, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 8733  
LENGTH: 378  
TYPE: PRT  
ORGANISM: Human  
US-09-949-016-8733

Query Match 1.5%; Score 11; DB 2; Length 378;  
Best Local Similarity 100.0%; Pred. No. 0.12;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 421 VPYLGTFITDL 431  
|||||  
Db 38 VPYLGTFITDL 48

## RESULT 9

US-10-118-328-5  
Sequence 5, Application US/10118328  
Patent No. 6773904  
GENERAL INFORMATION:  
APPLICANT: YAN, Chunhua et al.  
TITLE OF INVENTION: ISOLATED HUMAN RAS-LIKE PROTEINS,  
NUCLEIC ACID MOLECULES ENCODING THESE HUMAN RAS-LIKE  
PROTEINS, AND USES THEREOF  
FILE REFERENCE: CL001220  
CURRENT APPLICATION NUMBER: US/10/118,328  
CURRENT FILING DATE: 2002-04-09  
PRIOR APPLICATION NUMBER: 60/282,460  
PRIOR FILING DATE: 2001-04-10  
NUMBER OF SEQ ID NOS: 5  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 5  
LENGTH: 725  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-118-328-5

Query Match 1.5%; Score 11; DB 2; Length 725;  
Best Local Similarity 100.0%; Pred. No. 0.23;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 421 VPYLGTFITDL 431  
|||||  
Db 409 VPYLGTFITDL 419

## RESULT 10

US-08-408-519-2  
Sequence 2, Application US/08408519  
Patent No. 5955354  
GENERAL INFORMATION:  
APPLICANT: Williams, Lewis T.  
APPLICANT: Demo, Susan  
TITLE OF INVENTION: A No. 5955354el ras p21-Interacting Protein and  
USES THEREOF

1 ; NUMBER OF SEQUENCES: 5  
2 ; CORRESPONDENCE ADDRESS:  
3 ; ADDRESSEE: Townsend and Townsend Khourie and Crew  
4 ; STREET: 379 Lytton Avenue  
5 ; CITY: Palo Alto  
6 ; STATE: California  
7 ; COUNTRY: USA  
8 ; ZIP: 94301  
9 ; COMPUTER READABLE FORM:  
10 ; MEDIUM TYPE: Floppy disk  
11 ; COMPUTER: IBM PC compatible  
12 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
13 ; SOFTWARE: Patent In Release #1.0, Version #1.25  
14 ; CURRENT APPLICATION DATA:  
15 ; APPLICATION NUMBER: US/08/408,519  
16 ; FILING DATE: 20-MAR-1995  
17 ; CLASSIFICATION: 514  
18 ; ATTORNEY/AGENT INFORMATION:  
19 ; NAME: Dow, Karen B.  
20 ; REGISTRATION NUMBER: 29,684  
21 ; REFERENCE/DOCKET NUMBER: 02307K-56800  
22 ; TELECOMMUNICATION INFORMATION:  
23 ; TELEPHONE: 415-326-2400  
24 ; TELEFAX: 415-326-2422  
25 ; INFORMATION FOR SEQ ID NO: 2:  
26 ; SEQUENCE CHARACTERISTICS:  
27 ; LENGTH: 768 amino acids  
28 ; TYPE: amino acid  
29 ; TOPOLOGY: linear  
30 ; MOLECULE TYPE: protein  
31 ; US-08-408-519-2  
32  
33 Query Match 1.5%; Score 11; DB 1; Length 768;  
34 Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;  
35 Matches 11; Conservative 0;  
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37 QY 421 VPYLGTFLLTDL 431  
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39 Db 417 VPYLGTFLLTDL 427  
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1 ; INFORMATION FOR SEQ ID NO: 2:  
2 ; SEQUENCE CHARACTERISTICS:  
3 ; LENGTH: 768 amino acids  
4 ; TYPE: amino acid  
5 ; TOPOLOGY: linear  
6 ; MOLECULE TYPE: protein  
7 ; PCT-US95-03552-2  
8  
9 Query Match 1.5%; Score 11; DB 5; Length 768;  
10 Best Local Similarity 100.0%; Pred. No. 0.24; Mismatches 0; Indels 0; Gaps 0;  
11 Matches 11; Conservative 0;  
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13 QY 421 VPYLGTFLLTDL 431  
14 |||||  
15 Db 417 VPYLGTFLLTDL 427  
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RESULT 14  
US-08-820-170A-1

Sequence 1, Application US/08820170A  
Patent No. 5831058  
GENERAL INFORMATION:  
APPLICANT: Tsutomu, FUJIWARA  
APPLICANT: Takeshi, WATANABE  
APPLICANT: Masato, HORIE  
APPLICANT: Toyomasa, KATAGIRI  
TITLE OF INVENTION: HUMAN GENE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/820,170A  
FILING DATE:  
CLASSIFICATION: 536  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-820-170A-1

Query Match 1.3%; Score 9; DB 1; Length 122;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 TSQDKAPSV 643  
Db 16 TSQDKAPSV 24  
|||||

RESULT 15  
US-09-055-699-1  
Sequence 1, Application US/09055699  
Patent No. 6005088  
GENERAL INFORMATION:  
APPLICANT: Tsutomu, FUJIWARA  
APPLICANT: Takeshi, WATANABE  
APPLICANT: Masato, HORIE  
APPLICANT: Toyomasa, KATAGIRI  
TITLE OF INVENTION: HUMAN GENE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/055,699  
FILING DATE:  
CLASSIFICATION:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/820,170  
FILING DATE:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860  
TELEX: 6491103  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 122 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-055-699-1

Query Match 1.3%; Score 9; DB 2; Length 122;  
Best Local Similarity 100.0%; Pred. No. 3.2;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 TSQDKAPSV 643  
Db 16 TSQDKAPSV 24  
|||||

Search completed: June 12, 2006, 12:06:24  
Job time : 54 secs

APPLICANT: Zhao, Qing A.  
 APPLICANT: Wang, Jian-Rui  
 APPLICANT: Xue, Aidong J.  
 APPLICANT: Ren, Feiyan  
 APPLICANT: Wang, Dunrui  
 APPLICANT: Chen, Rui-hong  
 APPLICANT: Drmanac, Radolje T.  
 TITLE OF INVENTION: No. US20030096279A1el Nucleic Acids and  
 TITLE OF INVENTION: Poly peptides  
 FILE REFERENCE: 790CIP2D DIVA  
 CURRENT APPLICATION NUMBER: US/10/233,131  
 CURRENT FILING DATE: 2002-08-29  
 PRIOR APPLICATION NUMBER: 09/808,701  
 PRIOR FILING DATE: 2001-03-14  
 PRIOR APPLICATION NUMBER: 09/649,167  
 PRIOR FILING DATE: 2000-08-23  
 PRIOR APPLICATION NUMBER: 09/540,217  
 PRIOR FILING DATE: 2000-03-31  
 NUMBER OF SEQ ID NOS: 34  
 SOFTWARE: pt\_Fa\_genes Version 2.0  
 SEQ ID NO 33  
 LENGTH: 715  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-233-131-33

Query Match 68.6%; Score 487; DB 4; Length 715;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| Qy | 224 | DSSEACAE | EEGLMPQGLD | FSDEVAE | QTLIDLE | FSKVL | YEC | LGSV | MSQR | DRPG | 283 |
| Db | 229 | DSSEACAE | EEGLMPQGLD | FSDEVAE | QTLIDLE | FSKVL | YEC | LGSV | MSQR | DRPG | 288 |
| Qy | 284 | AAGASTV  | TRATVAQ    | NTVTC   | VLG     | SVL   | GAP | GLA  | APQ  | RAQ  | LEK |
| Db | 289 | AAGASTV  | TRATVAQ    | NTVTC   | VLG     | SVL   | GAP | GLA  | APQ  | RAQ  | LEK |
| Qy | 344 | RAILSALQ | SNPIY      | RLK     | RSW     | GA    | VS  | RE   | PL   | STFR | KLS |
| Db | 349 | RAILSALQ | SNPIY      | RLK     | RSW     | GA    | VS  | RE   | PL   | STFR | KLS |
| Qy | 404 | EEDNT    | PGSL       | KPP     | PG      | VP    | Y   | L    | G    | T    | F   |
| Db | 409 | EEDNT    | PGSL       | KPP     | PG      | VP    | Y   | L    | G    | T    | F   |
| Qy | 464 | QLO      | RRCQ       | SY      | TL      | SP    | HP  | PI   | LA   | AL   | HA  |
| Db | 469 | QLO      | RRCQ       | SY      | TL      | SP    | HP  | PI   | LA   | AL   | HA  |
| Qy | 524 | RLS      | AKL        | ARE     | KSS     | SG    | SG  | PG   | DP   | SS   | PT  |
| Db | 529 | RLS      | AKL        | ARE     | KSS     | SG    | SG  | PG   | DP   | SS   | PT  |
| Qy | 584 | PLS      | DL         | PS      | PR      | FP    | AL  | PL   | GS   | PR   | IP  |
| Db | 589 | PLS      | DL         | PS      | PR      | FP    | AL  | PL   | GS   | PR   | IP  |
| Qy | 644 | VRR      | ALQ        | KN      | V       | P     | Q   | W    | A    | C    | D   |
| Db | 649 | VRR      | ALQ        | KN      | V       | P     | Q   | W    | A    | C    | D   |
| Qy | 704 | TL       | S          | V       | S       | P     | S   |      |      |      |     |
| Db | 709 | TL       | S          | V       | S       | P     | S   |      |      |      |     |

RESULT 9  
 US-10-240-145-85  
 ; Sequence 85, Application US/10240145  
 ; Publication No. US20030235883A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hyseq, Inc

TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
 FILE REFERENCE: 21272-048  
 CURRENT APPLICATION NUMBER: US/10/240,145  
 CURRENT FILING DATE: 2002-09-27  
 PRIOR APPLICATION NUMBER: 09/540,217  
 PRIOR FILING DATE: 2000-03-31  
 PRIOR APPLICATION NUMBER: 09/649,167  
 PRIOR FILING DATE: 2000-08-23  
 PRIOR APPLICATION NUMBER: 09/668,680  
 PRIOR FILING DATE: 2000-09-22  
 PRIOR APPLICATION NUMBER: 09/695,618  
 PRIOR FILING DATE: 2000-10-23  
 PRIOR APPLICATION NUMBER: 09/728,711  
 PRIOR FILING DATE: 2000-11-30  
 PRIOR APPLICATION NUMBER: NOT YET ASSIGNED  
 PRIOR FILING DATE: 2000-03-14  
 NUMBER OF SEQ ID NOS: 172  
 SOFTWARE: Custom  
 SEQ ID NO 85  
 LENGTH: 715  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 US-10-240-145-85

Query Match 68.6%; Score 487; DB 4; Length 715;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 487; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

|    |     |          |            |         |         |       |     |      |      |      |     |
|----|-----|----------|------------|---------|---------|-------|-----|------|------|------|-----|
| Qy | 224 | DSSEACAE | EEGLMPQGLD | FSDEVAE | QTLIDLE | FSKVL | YEC | LGSV | MSQR | DRPG | 283 |
| Db | 229 | DSSEACAE | EEGLMPQGLD | FSDEVAE | QTLIDLE | FSKVL | YEC | LGSV | MSQR | DRPG | 288 |
| Qy | 284 | AAGASTV  | TRATVAQ    | NTVTC   | VLG     | SVL   | GAP | GLA  | APQ  | RAQ  | LEK |
| Db | 289 | AAGASTV  | TRATVAQ    | NTVTC   | VLG     | SVL   | GAP | GLA  | APQ  | RAQ  | LEK |
| Qy | 344 | RAILSALQ | SNPIY      | RLK     | RSW     | GA    | VS  | RE   | PL   | STFR | KLS |
| Db | 349 | RAILSALQ | SNPIY      | RLK     | RSW     | GA    | VS  | RE   | PL   | STFR | KLS |
| Qy | 404 | EEDNT    | PGSL       | KPP     | PG      | VP    | Y   | L    | G    | T    | F   |
| Db | 409 | EEDNT    | PGSL       | KPP     | PG      | VP    | Y   | L    | G    | T    | F   |
| Qy | 464 | QLO      | RRCQ       | SY      | TL      | SP    | HP  | PI   | LA   | AL   | HA  |
| Db | 469 | QLO      | RRCQ       | SY      | TL      | SP    | HP  | PI   | LA   | AL   | HA  |
| Qy | 524 | RLS      | AKL        | ARE     | KSS     | SG    | SG  | PG   | DP   | SS   | PT  |
| Db | 529 | RLS      | AKL        | ARE     | KSS     | SG    | SG  | PG   | DP   | SS   | PT  |
| Qy | 584 | PLS      | DL         | PS      | PR      | FP    | AL  | PL   | GS   | PR   | IP  |
| Db | 589 | PLS      | DL         | PS      | PR      | FP    | AL  | PL   | GS   | PR   | IP  |
| Qy | 644 | VRR      | ALQ        | KN      | V       | P     | Q   | W    | A    | C    | D   |
| Db | 649 | VRR      | ALQ        | KN      | V       | P     | Q   | W    | A    | C    | D   |
| Qy | 704 | TL       | S          | V       | S       | P     | S   |      |      |      |     |
| Db | 709 | TL       | S          | V       | S       | P     | S   |      |      |      |     |

RESULT 10  
 US-10-291-128-85  
 ; Sequence 85, Application US/10291128  
 ; Publication No. US20050202422A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Nuvelo, Inc  
 ; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
 ; FILE REFERENCE: 790CIP4